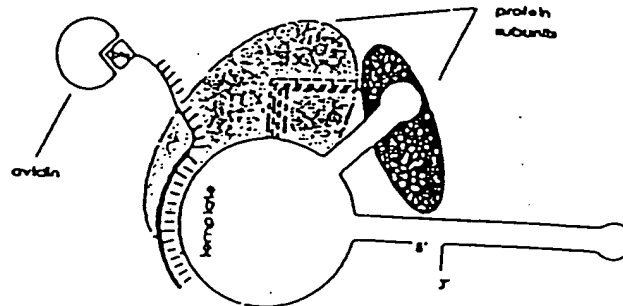


PANEL A



PANEL B

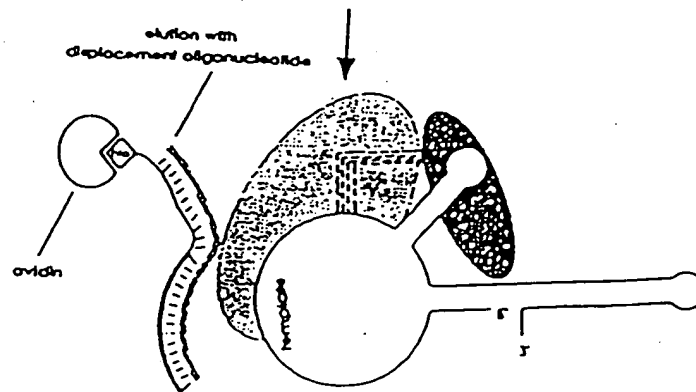


FIGURE 2

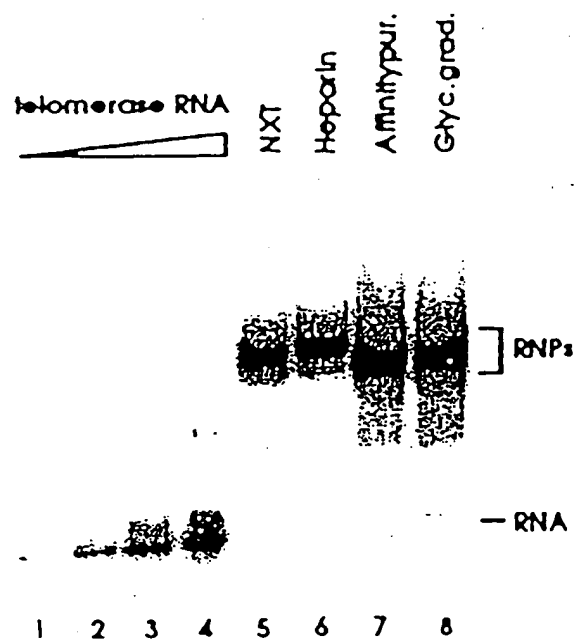


FIGURE 3

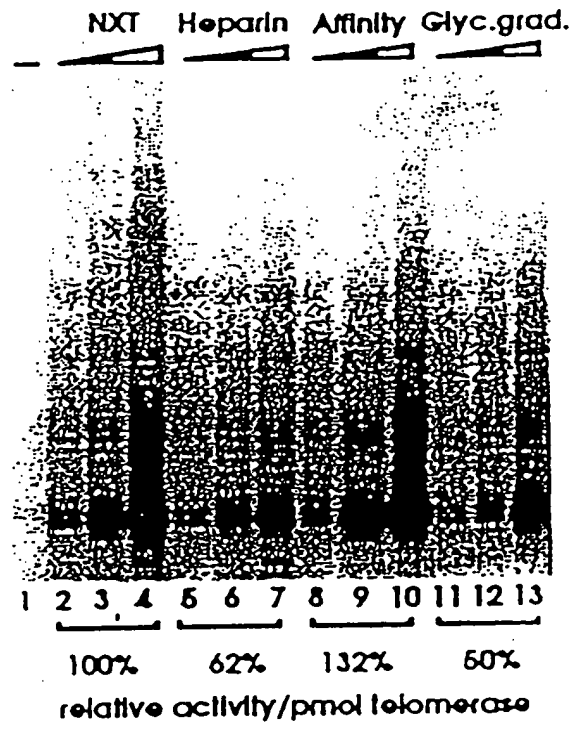


FIGURE 4

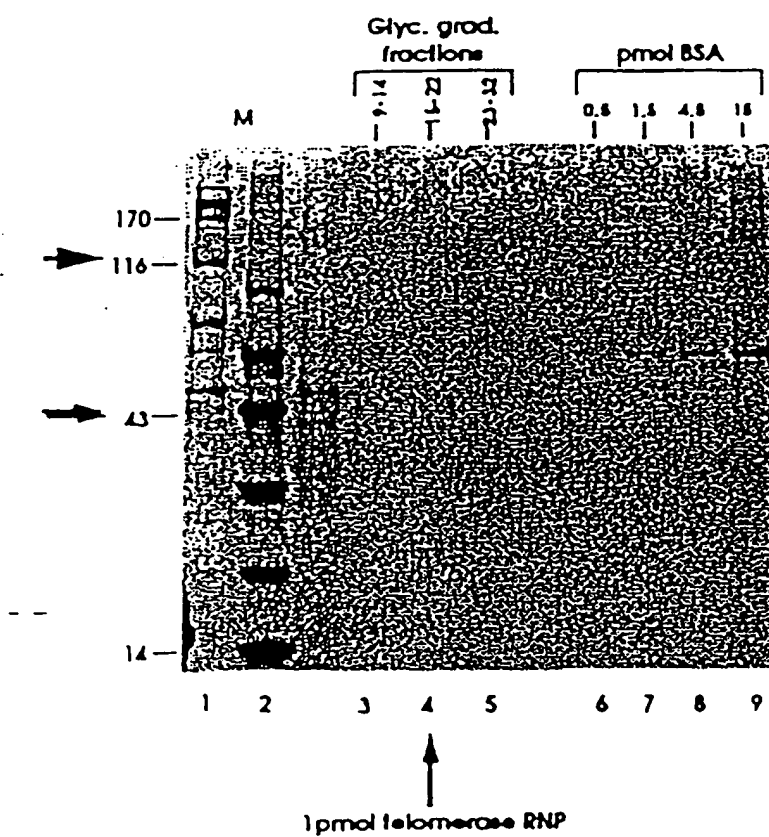
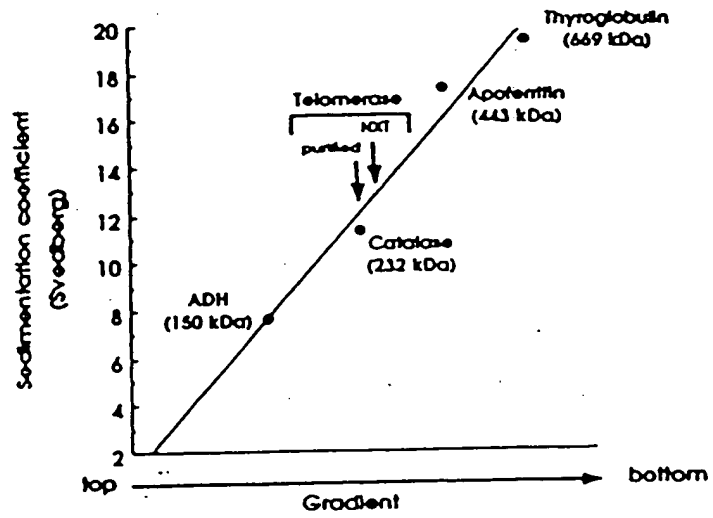


FIGURE 5



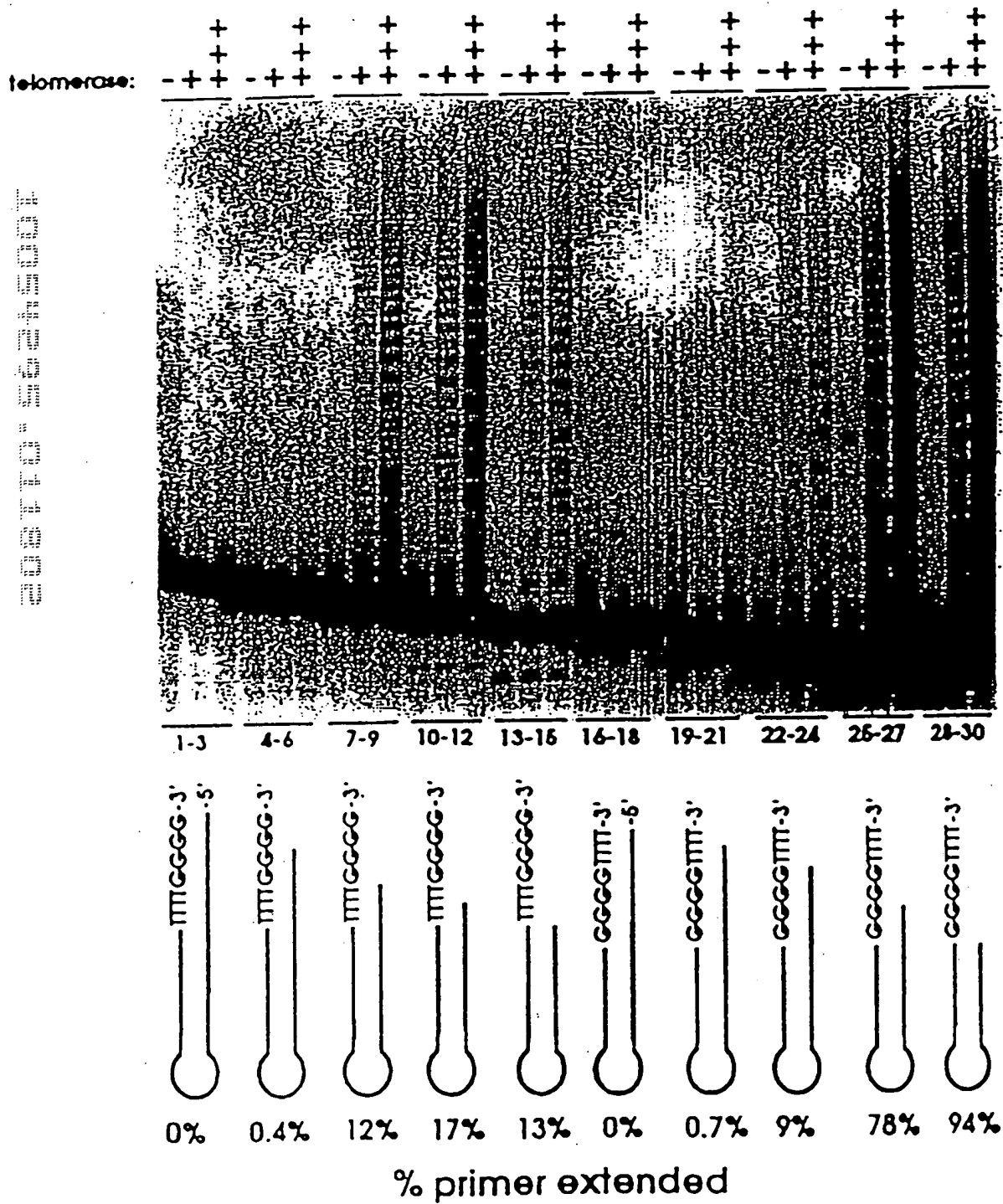



FIGURE 7

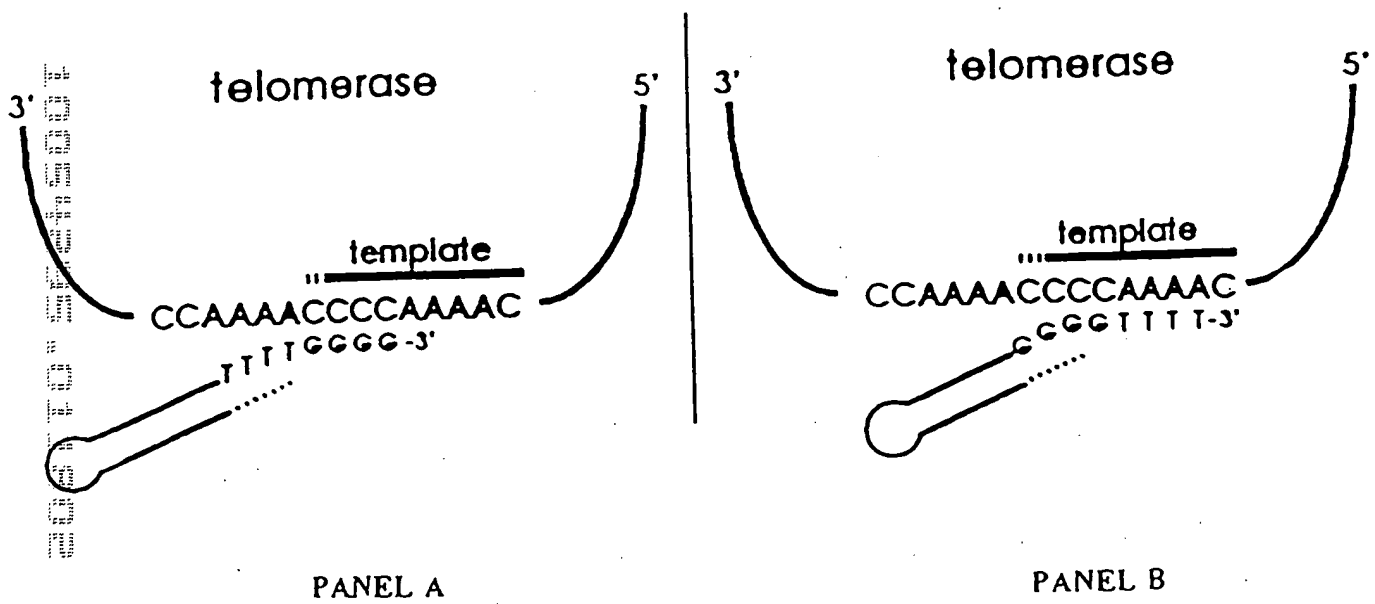


FIGURE 8

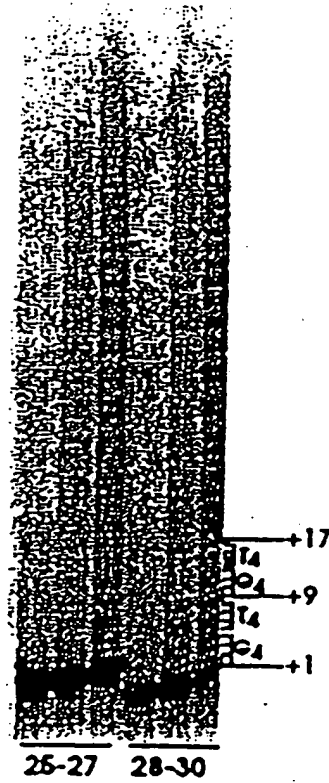


FIGURE 9

1 AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
 51 AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
 101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCACTCAGC
 151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGGA
 201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
 251 TTAGAAGATA TTAAATATT TGCGCAGACA AATATTGTTG CTA CTCCACG
 301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
 351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGA ACTTCTT
 401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC A
 451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
 501 CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
 551 ATTGGAAATG AGCTCTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
 601 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
 651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
 701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAT ACAATGTCAA
 751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
 801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT TAATAGAAAT
 851 AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTC
 901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
 951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
 1001 CTTGAGAAAG TCAAAGATTT TAACTTCAAC TACTATTTAA CAAAATCTTG
 1051 TCCTCTTCCA GAAAATTGGC GGGAACGGAA ACAAAAAATC GAAAACCTGA
 1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTTAGC
 1151 TACACAAC TG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA
 1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
 1251 AAAAGAAAGT TAAGAAATAT GTGGAAC TAA ACAAGCATGA ACTCATTCAC
 1301 AAAA ACTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
 1351 GGTTGAGACC TCTGCAAAGC ATTTTATTA TTTTGATCAC GAAAACATCT
 1401 ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT CGTCGTCTCG
 1451 CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
 1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
 1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
 1601 GAAGAATGGA AAAAGTCGCT TGGATTGCA CCTGGAAAAC TCAGACTAAT
 1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
 1701 TAAATTCAGA CCGGAAGACT ACAA AATTAA CTACAAATAC GAAGTTATTG
 1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
 1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
 1851 AGTTTGTGTTG CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTTGCA
 1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAA ACTATC
 1951 AACATTCTTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
 2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
 2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
 2101 TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
 2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
 2201 AGAAATTATT TTAAGAAAGA TAACTTACTT CAACCAGTCA TTAATATTG
 2251 CCAATATAAT TACATTA ACT TTAATGGGAA GTTTTATAAA CAAACAAAAG
 2301 GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGT CATC ATTTTATTAT

FIGURE 9 (cont.)

2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA
2401 CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451 TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501 ATAAACGTAA GTCGTGAAAA TGGATTAAAA TTCAATATGA AGAAACTACA
2551 GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601 GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651 TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751 CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTAATGAA TAACATTACC
2801 CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAACTCT
2851 CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901 AATACAAGGA CCACTTTAAG AAGAAGTTAG CTATGAGCAG TATGATCGAC
2951 TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051 ACTTTTTCTT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101 AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151 GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201 CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTTG TCTTATATAC
3251 TGGGGTTTTG GGGTTTTGGG GTTTTGGGG

FIGURE 10

1 MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
51 LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
101 SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
151 IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
201 ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNMKSRTTR IFYCTHFNRN
251 NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKCLK DKVIEKIAM
301 LEKVKDFNFN YYLTSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
351 YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELH
401 KNLLLEKINT REISWMQVET SAKHFYYFDH ENYVLWKLL RWIFEDLVVS
451 LIRCFYVTE QQKSYSKTY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
501 EEWKKS LGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
551 NSHMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
601 TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
651 FRKKEMKD YF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKT LIVEAKQ
701 RNYFKKD NLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
751 ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVL FIEKL
801 INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
851 SIDMKTLALM PNINLRIEGL CTLNLNMQT KKASMWLKKK LKSFLMNNIT
901 HYFRKTTITTE DFANKTLNKL FISGGYKYM CAKEYKDHFK KNLAMSSMID
951 LEVSKIISV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
1001 KYIFNRVCM LKAKEAKLKS DQCQSLIQYD A

FIGURE 11

1 CCCCAAACC CCAAACCCC AAAACCCCTA TAAAAAAGA AAAAATTGAG
 51 GTAGTTTGA AATAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
 101 TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
 151 GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
 201 TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
 251 CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
 301 AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
 351 AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
 401 TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTT
 451 CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
 501 GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
 551 AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCTG
 601 TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
 651 TTGAGACAAT TGAAAAAGCT GTTTACAAC GAAGGAATCG CAGTTCTGAA
 701 AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
 751 CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAATAAAC CATGCAAGTT
 801 TAATGGAATA TACGTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
 851 TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTAGC
 901 TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
 951 AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
 1001 TTGTTGATTCT TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
 1051 AAAGAAGAAG AGCTATCACA ATCCTGATTCT TAAAGATTT CAAAAATTC
 1101 AGGTAAGAGA GATACATTCA TTAATAATTCA TATATTATAG TTTTTCATTT
 1151 CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
 1201 GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
 1251 TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
 1301 GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
 1351 AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
 1401 AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
 1451 ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATT AAGAAATAAA
 1501 GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
 1551 CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
 1601 ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
 1651 AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
 1701 AAGATTTATT TTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
 1751 GGGGTTTTGG GG

FIGURE 12

1 CCCCCAACCCCAAAACCCCAAAACCCCTATAAAAAAGAAAAATTGAGGTAGTTTGA 60
 GGGGTTTGGGGTTTGGGGTTTGGGGATATTTTTTCTTTTTTAACCTCCATCAAATCT
 a P Q N P K T P K P L . K K K K L R . F R -
 b P K T P K P Q N P Y K K R K N C G S L E -
 c P K P Q N P K T P I K K E K I E V V . K -
 AATAAATATTATCCCGCACAAATGGAGATGGATATTGATTGGATGATATAGAAAATT
 61 TATTTTATAATAAGGGCGTGTACCTCTACCTATAACTAAACCTACTATATCTTTTAA 120
 a N K I L F P H K W R W I L I W M I . K I -
 b I K Y Y S R T N G D G Y C F G C Y R K F -
 c . N I I P A Q M E M D I D L D D I E N L -
 TACTTCTAATACATTCAACAAGTATAGCAGCTCTTGTAGTGACAAGAAAGGATGCAAAA
 121 ATGAAGGATTATGTAAGTTGTTTCATATCGTCGAGAACATCACTGTTCTTCTACGTTTT 180
 a Y F L I H S T S I A A L V V T R K D A K -
 b T S . Y I Q Q V . Q L L . . Q E R H Q N -
 c L P N T F N K Y S S S C S D K K G C K T -
 CATTGAAATCTGGCTCGAAATCGCCTTCATTGACTATTCCAAAGTTGCAAAAACAATTAG
 181 GTAAGTATGACCGAGCTTAGCGGAAGTAACTGATAAGGTTTCAACGTTTTTGTAAATC 240
 a H C N L A R N R L H C L F Q S C K N N . -
 b I E I W L E I A F I D Y S K V A K T I R -
 c L K S G S K S P S L T I P K L Q K Q L E -
 AGTTCTACTTCTCGGATGCAAAATCTTATAACGATTCTTCTTGAGAAAATTAGTTTTAA
 241 TCAAGATGAAGAGCTACGTTTAGAAATATGCTAAGAAAGAACTCTTTTAATCAAAATT 300
 a S S T S R M Q I F I T I L S C E N . F . -
 b V L L L G C X S L . R F F L E K I S F K -
 c F Y F S D A N L Y N D S F L R K L V L K -
 AAAGCGGAGAGCAAGAGTAGAAATTGAAACATTACTAATGTTTAAATAAAATCAGGTAA
 301 TTTCCGCTCTCGTTTCTCATCTTTAACTTTGTAATGATTACAAATTTATTTTACTCCATT 360
 a K A E S K E . K L K H Y . C L N K I R . -
 b K R R A K S R N C N I T N V . I K S G N -
 c S G E Q R V E I E T L L M F K . N Q V H -
 TGAGGATTATCTATTTTTTAGATCACTTCTTAAGGAGCATTATGGAGAAAATTACTTAA
 361 ACTCCTAATAAGATAAAAAATCTAGTGAAGAATTCCTCGTAATACCTCTTTTAATGAATT 420
 a C G L F Y F L D H F L R S I H E K I T . -
 b E D Y S I F . I T S . G A L W R K L L N -
 c R I I L F F R S L L K E H Y G E N Y L I -
 TACTAAAAGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAATT
 421 ATGATTTTCCATTGTCAAACTAATAAAGGGATCGGTTGTTACTACTCATATAATTAA 480
 a Y . K V N S L D Y F P S Q Q C C V Y . I -
 b T K R . T V W I I S L A N N D E Y I K F -
 c L K G K Q F G L F P . P T M M S I L N S -

FIGURE 12 (cont.)

CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAACTCGCTAT 540
 481 GTATACTCTTACTCAGTTTCTTAGAGCTATGTAGTCTGAATGTTTCTGTTTGAGCGATA
 a H M R M S Q R I S I H O T Y Q R Q T R Y -
 b I C E C V K G S R Y I R L T K D K L A I -
 c Y E N E S K D L D T S D L P K T N S L -
 AAAACCGAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTG 600
 541 TTTTGGCTTCTTTTCAAACCTATTAGCTTGTGCTCTTCTTGAATAACGTAATGATAAGC
 a K T O E K V C * S N S R R T Y C I Y Y S -
 b K R K K K F D N R T A E E L I A F T I R -
 c N A R K S L I I E Q Q K N L L H L L F V -
 TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACCTCCGAGTCTTGAGACAAT 660
 601 ATACCCAAAATAATGTTAAACAAATCCATAGCTGCCACTTGAGGGCTCAGAAGCTCTGTTA
 a Y G F Y Y N C F R Y R R C T P E S C D N -
 b H G F I T I V L G I D G E L P S L E T I -
 c W V L L Q L F * V S T V N S R V L R Q L -
 TGA AAAAGCTGTTTACAACCTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT 720
 661 ACTTTTTTCGACAAATGTTGACTTCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA
 a C K S C L Q L K E S Q F C K F * C V C H -
 b E K A V Y N C R N R S S E S S D V Y A I -
 c K K L F T T E G I A V L K V L M C M P L -
 TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAAACAAA 780
 721 ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT
 a Y F V N * S Q I S Y L N L M D S Y R N K -
 b I L C I N L K Y L I S I * W I A I E T N -
 c F C E L I S N I L S Q F N G * L * K Q T -
 CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC 840
 781 GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCTGTTTACGTGTG
 a P N K P C K F N G I Y V K S F G T N A H -
 b Q I N H A S L H E Y T L N P L G Q M H T -
 c K * T M Q V * W N I R * I L W D K C T L -
 TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC 900
 841 ACTTAAATATAACCTAAGCAATTTCTATCTATGTGCTTACGAAATCTCTGACTAAATCG
 a C I Y I G F L K H R Y T E C F R D C F S -
 b E F I L D S * S I D T Q N A L E T D L A -
 c N L Y W I L R A * I H R M L * R L I * L -
 TTACAACAGATTACCTGTTTGGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA 960
 901 AATGTTGCTTAATCGACAAAACCTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT
 a L Q Q I T C F D Y S C S S L I S L K E A -
 b Y N R L P V L I T L A H L L Y L * K K Q -
 c T T D Y L F C L L L L I S Y I F K R S R -
 GGCGAAATGAAAAGAACTAAAGAAAGAGATTTCAAATTTGTTGATTCTTCTGTAACC 1020
 961 CCGCTTACTTTTCTCTGATTCTTTCTCTAAAGTTTAAACAACCTAAGAAGACATTGG
 a G E M K R R L K K E I S K F V D S S V T -
 b A K C K E D * R K R F Q N L L I L L * P -
 c R N E K K T E R D F K I C C F F C N R -
 GGAATTAACAACAAGAAATATTAGCAACGAAAAAGAAGAGCTATCACAATCCTGATTTC 1080
 1021 CCTTAATGTTGTTCTTATAATCGTTGCTTTTCTTCTCTCGATAGTGTAGGACTAAG
 a G I N H K N I S N E K E E E L S O S C F -
 b E L T T R I L A T K K K K S Y H N P D S -
 c N * Q Q E Y * Q R K R R R A I T I L I L -

FIGURE 12 (cont.)

1081 TTAAGATTTCAAAAATCCAGGTAAGAGAGATACATTCATTAATAATTCATATATTATAG 1140
 AATTCTAAAGTTTAAAGGTCATTCTCTCTATGTAAGTAATTTAAGTATATAATATC
 a L K I S K I P G K R D T F I K I H I L -
 b R F Q K F Q V R E I H S L K F I Y Y S -
 c K D F K N S R E R Y I H N S Y I I V -
 1141 TTTTTCATTTCACAGCTGTTATTTTCTTTTATCTTAACAATATTTTGTAGTAGCTGGAA 1200
 AAAAGTAAAGTGTGACAATAAAAGAAAATAGAATTGTTATAAAAACTAATCGACCTT
 a F F I S Q L L F S F I L T I F F D L E -
 b F S F H S C Y F L L S Q Y F L I S W K -
 c F H F T A V I F F Y L N N I F C L A G S -
 1201 GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAAGTTAGCTTATTCACATTCAT 1260
 CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA
 a V K S I K E K R T E V T L I H I H -
 b K V S N K R S A R L R L S L F T F I -
 c K K Y Q I R E A L D C G N L A Y S H S -
 1261 AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTAAAAA 1320
 TCTAGCTGGAAGTATATAGGTTATGCTACTATTCTTTGTCGTCAGTAGGCAAAATTTT
 a R S T F I Y P I R C G N S S H P F K -
 b D R P S Y I Q Y D D K E T A V I R F K N -
 c I D L H I S N T M I R K Q Q S S V L K I -
 1321 TAGTGCTATGAGGACTAAATTTTAGAGTCAAGAAATCGAGCGAAATCTTAATCAAAAA 1380
 ATCAGGATACTCTGATTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTT
 a C Y E D I F R V K K W S R N L N O K -
 b S A M R T K F L E S R N G A E I L I K K -
 c V L C G L N F S Q E H E P K S S K R -
 1381 GAATTCGGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTGTTAATAAGTATTACCA 1440
 CTTAAGCGAGCTATAACGTTTCTTAGCTTGAGATTAGAAAGCAATTATTCATAATGGT
 a E L R R Y C K R I E L I F R V L P -
 b N C V D I A K E S N S K S F V N K Y Y Q -
 c I A S I L Q K N R T L N L S L I S I T N -
 1441 ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA 1500
 TAGAACTAACTAATTCTCTAACTGCTCCGTTGACGTGCTTCTAGTAATTTCTTTATT
 a I L I D C R D R C N C T E D H R N K -
 b S C L I E E I D E A T A Q K I I K E I K -
 c L D C L K R L T R Q L H R R S L K K S -
 1501 GTAACTTTATTAAATAGAGAATAAACTAAATTAATAATATAGAGATCAGCGATCTTCAA 1560
 CATTGAAAAATAATTAATCTCTTATTGATTAAATGATTATATCTCTAGTCGCTAGAAGTT
 a V T F I N R I N I T N I E I S D L Q -
 b L L L I R E T K L L I R S A I F N -
 c N F Y L E N K L N Y Y R D Q R S S I -
 1561 TTGACGAAATAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGCTCAAAAT 1620
 AACTGCTTTATTTTCGACTTCATTTCAATCTGTTATTTTATGTTTGAACCAGTTTAA
 a L T K K L N S T I K N T N L G Q N -
 b C R N X S C T K V R Q K I Q T L V K I -
 c D E I X A E L K L D N K K Y K P W S K Y -
 1621 ATTGACGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAATAAGGCAATAAAATAAATGA 1680
 TAACTCCTTCCTTTCTTCTGCTCAATCGTTTCTTTTATTCGTTATTTATTTTACT
 a I E E G X E D O L A K E K I R O I K C -
 b L R K E K K T S Q K K K G N K N E -
 c C G R K R R P V S K R K N K A I N K H S -

FIGURE 12 (cont.)

1681 GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTTCAATAATTTATTGAAAAGAGGGGTT 1740

CATGCTTCACTTCTTTATTTTCTAAATAAAAAAAGTTATTAAATAACTTTTCTCCCAA

a V Q K C R N K R F I F F N N L L K R G V -
b Y R S E E I K D L F F S I I Y C K E G F -
c T E V K K * K I Y F F Q * F I E K R G F -

1741 TTGGGGTTTTGGGGTTTTGGGG 1762

AACCCCAAAACCCCAAAACCCC

a L G F W G F G -
b W G F G V L G -
c G V L G F W -

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FIGURE 13

2 EVDNDHQAONHGIHSALKTC EEI KEAKTLYSWIQVIRCRNQSQSHYKDL 51
 19 ELELEMOENQNDIQVRVK... IDDPKQY... LVNVTAACLLQEGSYQDK 62
 52 EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF. STGLMIELIDKCLVELL 100
 63 DERRYITKALL... EVAESDPEFIQCLAVYIRNELYIRTTTNYIVAF. 107
 101 SSSDSRQKLOCFGFOLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM 150
 108 CVVHKNTOPFIEKYFNKAVLLPNDLLEVCEFAQVLYI 144
 151 IGNELEFRHLYTKYLIFORTSEGLVQFCGNNVFDHLKVNDKFDKKQKGA 200
 145 FDATEFNLY... LDRILSODIRKELTFRKCLQRCVRSKF 181
 201 ADMNE... PRCCSTCKYNVKNEDHFLNNINVPNNNMKSRTTRIFYCTHF 247
 182 SEFNEYQLGKYCTES... QRKKTFRYLSVTNKQKWDOTKKK... 220
 248 NRANQFFKKHEFVSNNKNNISAMDRAQTI FTNIFRFRIRKRLKDKVIEKI 297
 221 RKENLLTKLOATKESEDKSKRETG... DIMNVEDAIKALKPAVMKKI 264
 298 AYMLEKVKDFNFNYLT KSCPLPENWRERKQKIENLINKTREEKSKYEE 347
 265 AKRQNAWK... KHMKA PKIPNSTLESKYLTFKD 294
 348 LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKYVELNKHE 397
 295 LIKFCHISEP... KERVYKILGKKYPKTEEEYKAAFQDSASAPFN. PE 338
 398 LIHKNLLEKINTREISWMOVETSAKHFFYFDHENIYVLWKLRLWIFEDL 447
 339 LAGKMKIEISKWENELSAKGNTAEVWONLISSNQLPYMAHLRNLSN... 386
 448 VVSLRCFFYVTEQKSYSKTYYYRKNIDVIMKMSIADLKKETLAEVQE 497
 387 ILKAGVSD... 394
 498 KEVEEWKKS LGFAPGKRLRIPKKTFRPIMTFNKKIVNSDRKTTKLTTNT 547
 395 TTHS 398
 548 KLLNSHMLKLT LKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGPKL 597
 399 IVINK... ICEPKAVENSKM 415
 598 FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNIVID 647
 416 F... PLOFFSAIEAVN. EAVTKGFKAKK... RENMNLKGQIEAVKE... VVE 457
 648 SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKT LIVE 697
 458 KTDEEKKDM... ELEQTEGEFVKVNEGIGKQYINSIELAIK 496
 698 AKQRYNFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS 747
 497 IAVNKNLDEIKGHTAIFSDVSGSMSTSMGGAKKYGSVRTCLECALVLGL 546
 748 FYYATLEESSLGFLRDESMNPENPNVLLMRLTDDYLLITTQENNAVLFI 797
 547 MVKQRCES SFYIFSSPSSOCNKCYLEVDL... 576
 798 EKLINVSRENGFKFNMKK. LQTSFPLSPSKFAKYGHDSVEEQNIVQDYCD 846
 577 PGDEL RPSMOKLLQEKGLCGG... TDFPYECIDWTKNKTHVD 617
 847 WIGISIDMKTLALMPNINLRIEGILCTLNLMQTKKASHWLKKKLKSFLM 896
 618 NIVILSDMHIAEGYSDINVRGSSIVNSI... KKYKDEVN 653
 897 NNITHYFRKTTITTEDFANKTLNKLFI SGYKYHQCAKEYKD. HFKNLAM 945
 654 PNIKIF... AVDLEGY... KCLNLGDEFNENNYIKIFGM 687
 946 SSHIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFI 995
 688 SDSI... LKFISAKQGA... NMVE 706
 996 IFSTKKYIFNRVC 1008
 707 VI... KNFALQKIG 717

FIGURE 14

132 LSTOKQYFFODEWNOVRAHIGNEL.FRHLYTKYLIFORTSE..GTLVQFC 178
 1 MSRRNQ.....KKQAPIGNETNLDFVLQNLLEVYKSQIEHYKTQOOOI 43
 179 GNNVFDHLKVNDKFDKKQKGAADHNEPRCCSTCKYNVKNKDHFLNNIN 228
 44 KEEDLKLLKFKNQDQDGNNGNDDDDDEE.....NNSNQQLLRRVN 84
 229 VPNNWNHKSRTTRIFYCTHFNRRNQFFKKHEFVSNKNNISAMDRAQTIFTN 278
 85QIKQOVQLIKK...VGSKEKDLNLDNEDENKKN 114
 279 IFRFNRIKKLKDVKIEKIAHYMLEKVDFNFNYLTKSCPLPENWRERKQ 328
 115 GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRET DY 164
 329 KIENLINKTREETSKYEEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
 165 DTEKWFIEISHDQK.....NYVSIYANQKTSYCWWLKDYFNK 200
 378 RNRKNFQKKVKYVELNKHLEIHNKLLLEKINTREISWMQVETSAKHFY 427
 201 NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID..... 242
 428 FDHENIYVLWKLLRWI..FEDLVVSLIRCFYVTEQQKSYSKTYYYRKN 475
 243 VNFQNNLCILALLRFLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290
 476 WDVIMKHSIADLKKETLAEVQKEVEEWKSLGFAFGKLRLLPKTTFRP 525
 291 FAVVFSHR.....HLQGIHLQVPCFAFYLVNSSSQISVKDSQLO 330
 526 IMTFNKKIIVNSDRKTTKLTNTKLLNSHMLKTLKNRMFKDPFGFAVFNY 575
 331 VYSFSTDLKLVD..TNKVQDYFKFLQEFPRLTHVSQAIPVSATNAVENL 378
 576 DDVMKKYEEFVCKWKQVQPKLF.....FATHDIEKCYDS..VNREK 615
 379 NVLLKKVKH..ANLNLVSIPTQFNDFYFVNQLHLKLEFGLPEPNILTKQK 426
 516 LSTFL.....KTTKLLSSDFWIMTAQILKRKNNI..VIDSKNFRKKEHK 657
 427 LENLLLSIKOSKNLFLRLNFYTYVAQETSRKQILQATTIKNLKNNKNO 476
 558 DYFRQKFQKIALEGGQYPTLFSVLEN..EQNDLNAKKTLLIVEAKQRNYFK 705
 477 EETPETKDETPESTSGHKFFDHLSELTELEDFSVN....LQATQEIY 520
 706 KDNELQPVINICQYNYINFNGKFYKOTKGIPOGLCVSSILSSFYATLEE 755
 521 ..DSLHKLLIRSTNLKKFKLSYKYEKSKMDTFIDLKNI.....YETLNN 564
 756 SSLGLRDESKNPNPNVNLHRLTDDYLLITTOENNAVLFIKLINVSR 905
 565LKRCNVISNPHGNISYELTN.....KDSTFYKFKLTNLQE 500
 806 ENGFKFNMKKLQTSFPLSPSKFAKYCHDSVEEQNIVQDYCDWIGISIDMK 855
 501 LQAKYTFK..QNEFQFNNVKSAKIESSSLESLEDIOSLCKSIASCKNLQ 648
 856 TLALMPNINLRIEGILCTLNLMQT..KKASMWLKK..KLKSFLMNNITH 901
 649 NVNI.....IASLLYPNNIQKNPFNKPNNLLFFKQFEQLKNLENVSINC 691
 902 YFRKTI.....TTEDFANKTLNKLFISSGGYKYMOCAYEKDHFKNLAMSSH 948
 692 ILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFTLQQLPEL 741
 949 IDEVSKIISVT.....RAFFKYLVCNIKDT..IFGEEHY 982
 742 NQYVINQQLLEELTVSEVHKQVWENHKKQAFYEPLCEFIKESSQTLQIDF 791
 983 PDFFLS..TLNHFIEIFSTKKY IFNRVCHILKAKEAKLKSODOCSLQ 1028
 792 DQNTVSDDSIKKILESISESKYHHYLRNPSQSSSLIKSENEETQELLK 840

FIGURE 15

[illegible]

[illegible]

FIGURE 17

	Motif A	Motif B
Consensus	h--h <h>h</h> h---h--h	h---- <h>h</h> h---h
telomerase p123	GQPKLFPATMDIEKCYDSVNREKLSFLKTKLL-100-RFYKQTKGIF <h>h</h> LCVSSILSSFFYATLEZSSLGFL	h---- <h>h</h> h---h
Dong (LINE)	KVRNLHCTYIDYKKAADSIPHSVLIQVLEIYKIN-28-RQLAIKKGIY <h>h</h> DSLSPLWFCALNPLSHQLANDR	h---- <h>h</h> h---h
al S.c.(groupII)	FGGSNWFREVDLKKCFDTISHDLIIKELFRYISD-26-HVPVGPVRVCV <h>h</h> CAPTSPALCNVAVLRLORRLAGLA	h---- <h>h</h> h---h
HIV-RT	LKKKRSVTVLGVGDAYFSVPLDEDFRKYTAFTIP-7-GIRYQYNVLP <h>h</h> GMKGSPIAFQSSMTKILEPFRKQN	h---- <h>h</h> h---h
L8543.12	VLPELYFMKFLVXSCYDSIPRMECMRILKDALKN-68-KCYIREDEGLF <h>h</h> ESSLSA?IVDLVYDDLLLEFYSEPK	h---- <h>h</h> h---h

	Motif C	Motif D	Motif E
Consensus	h--Y <h>h</h> DD <h>h</h> h	<h>h</h> h-h-- <h>h</h>	h-h <h>h</h> h-h
telomerase p123	-14-LMRLLTDDYLLITTTQENN-0-AVLFIKRLINVSRENCFKYNMRLQT-23-QDYCDWIGISL	<h>h</h> h-h-- <h>h</h>	h-h <h>h</h> h-h
Dong (LINE)	-16-HLIYMDIILKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLKCKT-25-KCYKYLGFQQ	<h>h</h> h-h-- <h>h</h>	h-h <h>h</h> h-h
al S.c.(groupII)	-55-YVRYADDIILIGVLGSKN-2-KIKRDLNLFNSLGLTINEERTLI-4-ETPARFLGYNL	<h>h</h> h-h-- <h>h</h>	h-h <h>h</h> h-h
HIV-RT	-4-IYQYMDLLYVGSHEIG-1-HRTKTEELRQHLRLRWGLTTPDRKHOK-0-EP?FLWYGYEL	<h>h</h> h-h-- <h>h</h>	h-h <h>h</h> h-h
L8543.12	-8-ILKLADDFLIISTDQQQ.....VINIKKLAMCGFQKYNANR-41-IRSKSSKGIIFR	<h>h</h> h-h-- <h>h</h>	h-h <h>h</h> h-h

FIGURE 18

telomerase p43	LQKQLEEFYFSDANLYNDSEFLRKLVLKSGEQRVEIETLLM
human La	ICHQDEYFEGDFNLPRDKELKEQI.KLDEGWVPLEIMIK
Xenopus LaA	ICEQDEYFEGDFNLPRDKELKQOI.LLDDGWVPLETMIK
Drosophila La	ILRQDEYFEGDANLNPRDKELREQIGKNEDGWVPLSVLVT
S. c. Lhplp	CLKQDEYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT

FIGURE 19

1 aactcatta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
 61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagtt agggtaaga ttgacgatcc taagcaatat ctctggaacg tcaactgcagc
 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt ctgaggtgg ctgagtcga tctgagttc atctgctagt tggcagtcata
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat ttgtgttgt
 421 ccacaagaat actcaacct tcatcgaaaa gtacttcaac aaagcagtac tttgcctaa
 481 tgacttactg gaagtcgtg aatttgcata ggttctctat attttgatg caactgaatt
 541 caaaaattg tatctgata ggatacttc ataagatatt cgtaaggaac tcactttccg
 601 taagtgtta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaatctgaag ataagtcaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tccfaactct acctggaat caaagtactt
 961 gaccttcaag gatctcata agttctgcca tatttctgag cctaaagaaa gagtctataa
 1021 gatccttggg aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
 1081 tgcactgca ccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
 1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataattaat
 1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
 1261 cgggttttca gatactacac actctattgt gatcaacaag attgtgagc ccaaggccgt
 1321 tgagaactcc aagatgttc ccttcaatt ctttagtgcc attgaagctg ttaatgaagc
 1381 agttactaag ggattcaagg ccaagaagag agaaaatag aatcttaaag gtcaaatcga
 1441 agcagtaag gaagtgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
 1501 aaccgaagaa ggagaatttg ttaagtcaa cgaaggaatt ggcaagcaat acattaactc
 1561 cattgaactt gcaatcaaga tagcagttta caagaattta gatgaaatca aaggacacac
 1621 tgcaatctc tctgatgtt ctggttctat gactacctca atgtcaggtg gagccaagaa
 1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggttga tggtaaaata
 1741 acgttgtaa aagtcctcat tctacatctt cagttcacct agtttcaat gcaataagtg
 1801 ttacttagaa gtgaltcc ctggagacga actccgtct tctatgtaa aacttttgca
 1861 agagaagga aaacttggg gtggtactga ttccctctat gattgcattg atgaatggac
 1921 aaagaataaa actcacgtag acaataatct tatttgtct gatagatga tgcagaagg
 1981 atattcagat atcaatgtta gaggcagtc cattgttaac agcatcaaaa agtacaagga
 2041 tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgcct
 2101 taatctaggt gatgagtca atgaaaacaa ctacatcaag atattcggtg tgagcgattc
 2161 aatctaaag ttactttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
 2221 cttgcccct caaaaaatag gacaaaagtg agtttctga gattcttcta taacaaaaat
 2281 ctcacccac ttttggtt tattgcatag ccattatgaa atttaaatta ttatctatt
 2341 atttaagta ctacatagt ttatgtatcg cagtcattta gcctattcaa atgattctgc
 2401 aaagaacaaa aaagattaaa a

FIGURE 20

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYQDKDERRYIITKALLEVAESDPEFICQLAVYIRNELYIRTTTN
YIVAFCVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYIFDATEFKNLYLDRILS
QDIRKELTFRKCLQRCVRSKFSEFNEYQLGKYCTESQRKKTMTFRYLSVTNKQKWDQTK
KKRKENLLTKLQAIKESEDKSKRETGDIMNVEDAIAKALPAVMKKIAKRQNAMKKHMK
APKIPNSTLESKYLTFKDLIKFCHISEPKERVYKILGKKYPKTEEEYKAAFSDSASAP
FNPELAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGV
SDTTHSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKRENMNKKGQIE
AVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIGKQYINSIELAIAVNKNLDEIKG
HTAIFSDVSGSMSTMSGGAKKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQ
CNKCYLEVLDLPGDELPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHTVDNIVILSD
MMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKJFAVDLEGYGKCLNLGDEFNENNYI
KIFGMSDSILKFISAKQGGANMVEVIKNFALQKJGQK

FIGURE 21

1 tcaatactat taattaataa ataaaaaaaa gcaaaactaca aagaaaatgt caaggcgtaa
 61 ctaaaaaaaaag ccataggctc ctataggcaa tgaacaaat ctgtatttg tattacaaaa
 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
 181 ggaggatctc aagcttttaa agtcaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgatgatgat gaagaaaaca actcaataa ataataagaa ttattaagga gagtcaatta
 301 gattaagtag caagttaat tgataaaaa agttggttct aaggtagaga aagatttgaa
 361 ttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aatagggtta gtattaaaat ttagtattta acatggacta
 481 ccagttgat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa ttacgcca
 601 ctaaaagaca tcatttgtt ggtggcttaa agattatgtt aataaaaaa attatgatca
 661 tcttaatgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
 721 ttcacaaaca atcaactta ctaataattc ttactagact gtaacatag acgttaattt
 781 tgataataat ctctgtatc tcgcattgct tagattttta ttactactag aaagattcaa
 841 tattttgaat ataagatctt cttatacaag aaattaatat aattttgaga aaattgggtga
 901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt
 961 acaagttcct tgcgaagcgt tctaatttt agttaactcc tcatcataaa ttacggttaa
 1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaaca
 1081 agtccaagat tattttaagt tcttataaga attcctcgt ttgactcatg taagctagta
 1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt
 1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
 1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
 1321 aaagcttgaa aatctacttt tgagtataaa ataatacaaa aatcttaaat ttttaagatt
 1381 aaacttttac acctacgttg ctaagaaac ctccagaaaa cagatattaa aacaagctac
 1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaagatga
 1501 aactccaagc gaaagcaca gtggtatgaa atttttgat catctttctg aattaaccga
 1561 gcttgaagat ttacgctgta acttgtaagc tacccaagaa atttatgata gcttgcacaa
 1621 acttttgatt agatcaacaa atttaagaa gticaaatta agttacaaat atgaaatgga
 1681 aaagagttaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
 1741 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttctatg aactgacaaa
 1801 taaagattct acttttata aatttaagct gaccttaac taagaattat aacacgctaa
 1861 gtatacttt aagtagaacg aatttaatt taataacgtt aaaagtgcaa aaattgaatc
 1921 ttccatcta gaaagcttag aagatattga tagtctttgc aaatctattg ctcttgtaa
 1981 aaattacaa aatgttaata ttatcgccag ttgctctat cccaacaata tttagaaaaa
 2041 tccittcaat aagcccaatc ttctatttt caagcaattt gaataattga aaaatttga
 2101 aaatgtatct atcaactgta ttctgatca gcatatactt aattctattt cagaattctt
 2161 agaaaagaat aaaaaataa aagcattcat ttgaaaaga tattatttat tacaatatta
 2221 tcttgattat actaaattat taaaacact tcaatagta cctgaattaa attagttta
 2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
 2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaacc
 2401 cctttagcta atagattttg accaaaacac tgaagtgtat gactctatta aaaagattt
 2461 agaattcata tctgagtcta agtatcatca ttatttgaga ttgaacccta gtaattctag
 2521 cagtttaatt aaatctgaaa acgaagaat ttaagaactt ctcaaagctt gcgacgaaaa
 2581 aggtgttta gtaaaagcat actataaatt cccctatgt ttaccaactg gtacttatta
 2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaataaa tattaatat
 2701 tgaatattc ttgcttatt attgaataa tacatacaat agtcaattt agtgtttga
 2761 atataattta gttatttaatt tcattatttt aagtaataa ttattttca atcattttt
 2821 aaaaaatcg

FIGURE 22

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQIK
EEDLKLLKFKNQDQDGNNGNDDDEENNSNKQQELLRRVNQIKQQVQLIKKVGSKVEK
DLNLNEDENKKNGLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRR
ETDYDTEKWFEISHDQKNYVSIYANQKTSYCWWLKDYFNKNNDHLNVSINRLETEAE
FYAFDDFSQTIKLTNNSYQTVNIDVNFNNLCILALLRFLSLERFNILNIRSSYTRN
QYNFEKIGELLETFVVFVSHRHLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQVYSF
STDLKLVDTNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNL
VS IPTQFNFDYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNLKFLRLNFTY
VAQETSRKQILKQATTIKNLKNNKNQEETPETKDETPSESTSGMKFFDHLSELTELED
FSVNLQATQEIYDSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLK
RCSVNISNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFNNVKSAKIE
SSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNPFNKPNNLLFFKQFEQLK
NLENVSINCILDQHILNSISEFLEKNKKIKAFILKRYLLQYYLDYTKLFKTLQQLPE
LNQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSTLQLIDFDQNTVSD
DSIKKILESISESKYHHYLRNLNPSQSSSLIKSENEEIQELLKACDEKGVLVKAYYKFP
LCLPTGTYDYDYNDRW

FIGURE 23

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL

PNSRKIALPCLPGDL SHKAVIDHCIIYLLTGELYNNVLTFGYKIARNEDVNNSLFCHS

ANVNVTLKGAAWKMFHSLVGTYAFVDLLINYTVIQFNGQFFTQIVGNRCNEPHLPPK

WVQRSSSSSATAAQIKQLTEPVTNKQFLHKLNNSSSFFPYSKILPSSSSIKKLTDLR

EAIPTNLVKIPQRLKVRJNLTLQKLLKRHKRLNYVSILNSICPPLEGTVLDLSHLR

QSPKERVLFHIVILQKLLPQEMFGSKKNKGKIIKNLNLNLLSLPLNGYLPFDSLLKKL

RLKDFRWLFISDIWFTKHNFNENLNQLAICFISWLFRLIPKIIQTFFYCTEISSTVTI

VYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLNHNHSMRIIPKKSNNEFR

IIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKE

FKQRLKKKFNNVLPELYFMKFVDKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFN

TNTGVLKLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY

IREDGFLFQGSSLSAPIVDLVYDDLLEFYSEFKASPSQDTLILKLADDFLIISTDQQQV

INIKKLAMGGFQKYNANRDKILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMN

NFHRSKSSKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISECYKSAF

KDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIEYEVRFILNGFLESLSNTS

KFKDNIILLRKEIQHLQAYIYIYIHIVN

FIGURE 24

Oxytricha
Euplotes

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIGURE 25

human
t z1
EST2
p123

Motif 0

AKPLHWLMSVYVVELLRSPFYVTETTFQKNR
ISEIEWLVLGKRSNAXMCLSDFEKRRQIFAEFIYWLNSPIIPILQSFFYITESDLNR
LKDFRWLFISD---IWFTKHNFFENLNQLAICFISWLPRLPKIIQTFFYCTEISSVT-
TREISWMQVET-SAXHPYYFDHEN-IYVLWKLRLRWIFEDLVVSLIRCFFYVTEQQKSYSK
*

Motif 1

human
te21
EST2
p123

LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHRARPALLTSRLRPFKP--DGL
TVYFRKDIWKLRCRPI-TSMKMEAPEKINENNVRMDTQK-TTLPPAVIRLLPKK--NTP
IVYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSTLS--HFNHSMRIIPKSNNEF
TYYYRKNIDVIMKMSI-ADLKKETLAEVQEKEVEWKKK-LGFAPGKLRLIPKK--TTF
* *

Motif 2

human
t z1
EST2
p123

RPIVNM DYVVGARTFRREKRAERLTSRVKALP-SVLNYERA
RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLIN EESSGIPFNLEVYHKLTF
RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
RPIMTFNKKIVNSDRKTTKLTNTKLLNSHLMKTLKN-RMFKDPFGPAVFNYDDVMKKY
* *

Motif 3 (A)

te21
EST2
p123

KKDLLKHRMFOR-KKYFVRIDIKSCYDRIKQDLMPRIVKK-KLKDPEPVIRKYATIHATS
KQRLKKFNVLPELYFMKFDVKSCYDSIPMECHRIKLD-ALKNENGFFVRSQYFPNTN
KEFVCKWKQVGQPKLPFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN
* *

FIGURE 26

[illegible]

FIGURE 27

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKS VWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHQREARPA LLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKR
AERLTSRVKALFSVLNYERA

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FIGURE 28

[illegible]

FIGURE 29

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLV
STFPNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRK
RTIETSITQNK SARKEVSWNSISIRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMLQWIFPRQFG
LINAQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRJFEILKDLETFLKLSRYESFSLHYLMSNIKISEIEWLVL
GKRSNAKMCLSDFEKRKQIFAEFIYWL YNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCRPFIT
SMKMEAFEKINENNVRMDTQKTTLP PAVIRLLPKKNTFRLITNLKRFLIKMGSNKKMLVSTNQT
LRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGGRKKYFVRIDIKSCYDRIKQDLMFR
IVKKKLLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVDLDFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRLDITLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCNI
YRLGYSMCMRAQAYLKRMDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFLHRRJAD

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FIGURE 30

ggtaccgattactttcttctcataagctaattgcttctcgaacgctcctaatactcttgaaatattttacaagaactcaataacaalaccaagtc aaattccaatatgaagg
tgtatttagtgcgataaiaatttctatttalcgggtcgttaccagataaaggacaaaaagaacacttccctccctaaagacttttactttaatttacttttcaaatatttcg
ggttcgttacttttaacggtgactgttttagctgctacttctagccaaccggtgttttctaccccgctcattggatatagctcttggagtagctcacagaaatccttacaatctt
ctgatgagactatattagattcattacagtcggtgcatattcttaacatggagccttacacttttagatgagtcacgctgcatgatggagtattggatcatccaacgtttgccttg
aaaaggttgataaattattgcaaaatcatgiccttagtgggtgtaatccgcgaaagtttttgatgctgcacacgcttagcatgattgagatattcaaaaattctatccactaca
ctccttaacgcgggtttattttctatttctatttctatgttggcctcaaatatgtatcatctcgtattaggtcttttccgttttactcctggaatcgtaccttttactattccccctaag
aataatctaaattagtttcgtataaattagatagtagtaaaagattgggtacttactcgtgtaattgttattagtttaagatactttgcaaaacatttattagctatcattatataaaa
aaaatcctataattataaataatcaatatttgcggtcactatttattaaacggttagatcagtaggacactttgcatatatagttatgcttaattggttactgttaacttgcAT
GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTA
CCTTAAATGATTATGTACAACTTGTGTTTGAAGGGTGC GCCGCAAGCTCGTATAGCAATATATGCGAA
CGCTTGAGAAGCGATGTACAAACGTCCTTTTCTATTTTCTTTCATTGACTGTAGTCGGCTTCGACAGT
AAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAAATGCTCACAGTCAGAGgtatatattttgtttgattttttctattcg
ggatagctaataatagggcagCTAATAGCGAATGTTGTAAAACAGATGTTTCGATGAAAGTTTTGAGCGTCGAAGGA
ATCTACTGATGAAAGGGTTTTCCATGgtaaggtattctaattgtgaataatttacctgcaattactgtttcaagagattgtatttaaccgataaagAA
TCATGAAGATTTTCGAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCTAATTA
CCTTATATCTATACTTGAGTCAAAAAAATTGGCAACTTTTGTAGAAAATgtaaataccggtaagattgttcgcactttgaa
agactgacaagtatagTATCGGCAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTGAAGGCTCTTC
CAAATGACAATTACCTTCAGATTTCTGGCATACCACTTTTTAAAAATAATGTGTTTGAGGAACTGTGT
CAAAAAAAGAAAGCGAACCATTGAAACATCCATTACTCAAAAATAAAAGCGCCCGCAAGAAGTTTC
CTGGAATAGCATTTCATTAGTAGGTTTAGCATTTTTTACAGGTCATCCTATAAGAAGTTTAAAGCAAGgt
aactaatactgttatccttcataactaatttagATCTATATTTTAACTTACACTCTATTTGTGATCGGAACACAGTACACATG
TGGCTTCAATGGATTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAGCAATTGCACAA
AGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCCTCTAAAGGTATACCTTTAATTGA
ACAAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAAGTTTACAACCATTATTGCCCATATATTGA
CACCCACGATGATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATC
CATTCTTGTTGAGTGTTTCTCTAAATTAATCTGGGGTAACCAAGGATATTTGAGATAATATTAAAGg
tattgtataaaatttattaccactaacgattttaccagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTAC
ATTATTTAATGAGTAACATAAAAGgtaatatgcaaattttttaccattaattaacaatcagATTTTCAGAAATTGAATGGCTAGT
CCTTGGA AAAAGGTCAAATGCGAAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAATATTTGCGG
AATTCATCTACTGGCTATACAATTCGTTTATAATACCTATTTTACAATCTTTTTTTTATATCACTGAATC
AAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTTGAAAACCTTTGTGCCGACCCTTTAT
TACATCAATGAAAATGGAAGCGTTTGAAAAAATAAACGAGGgtattttaaggtatttttgcaaaaagctaattttcagAACAA
TGTTAGGATGGATACTCAGAAAACACTTTGCCTCCAGCAGTTATTCGTCTATTACCTAAGAAGAATAC
CTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAAGgtattaattttggcatcaatgtacttacttctaatctattattag
cagATGGGTTCAAACAAAAAATGTTAGTCAGTACGAACCAAACCTTTACGACCTGTGGCATCGATACTG
AAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGAGGTTTACATGAAGCTTCTTACT
TTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGGgttaattataatgctgctcatttattatttgcagCGTAAGAAG
TATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATTGTT
AAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATAACATGCAACAAGTGACCG
AGCTACAAAAAATTTGTTAGTGAGGCGTTTTCTATTgtaagttatttttattggaatttttaacaaattcttttagTTGATAT
GGTGCTTTTGA AAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTGATTGTTGT
GGATTATTGGACCAAAAGTTCTTCTGAAAATTTTAAAAATGCTCAAGGAACATCTCTCTGGACACATTGT
TAAGgtataccaattgtgaattgtaataacactaatgaaactagATAGGAAATTTCTCAATACCTTCAAAAAGTTGGTATCCCTC
AGGGCTCAATTCTGTCTCTTTTTTGTGTCATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTT
TACGAAAAAGAAAGGATCAGTGTTGTACGAGTAGTCGACGATTTCTCTTTATAACAGTTAATAAAA
AGGATGCAAAAAAATTTTTGAATTTATCTTTAAGAGgtgagttgctgtcattcctaagttctaaccgtgaagGATTTGAGAA
ACACAATTTTTCTACGAGCCTGGAGAAAACAGTAATAAACTTTGAAAATAGTAATGGGATAATAACA
ATACTTTTTTTAATGAAAGCAAGAAAAGAATGCCATTCTTCGTTTCTCTGTGAACATGAGGTCTCTTG
ATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAGAGCTGACGAAAC
ATATGGGGAAATCTTTTTTTTACAAAATTTCTAAGgtatactgtgaactgaataatagctgacaaataatcagATCGAGCCTTGC
ATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAAATTTCAATTCTTGCTGCAATATATATAG
GCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTTCCC
AAAGAATGTTTCATAACGGgtgagttacttatttaactagaaaagtcattaattaaccttagATCTTTTGAATGTTATTGGAAGAAAA
ATTTGGA AAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCCTCTGCAGAAGTCAA

[illegible]

FIGURE 31

EST2 pep	FFYCTEISST	VIVYFRHDT	WN----	KLIT	P-----	FIVE	YFK-TYLVEN	40
Euplotes pep	FFYVTEQQKS	YSKTYYYRKN	IWDVI-MKMS	IAD----	LKK	ETLA--EVQE		43
Trans of tetrahymen	-----KHKE	GSQIFYRKP	IWKLVSCLTI	VKVRIQFSEK	NKQMKNNFYQ			44
Consensus	FFY.TE..K.	.S..YYRK.	IW...-KL..-F..KV..			50
EST2 pep	NVCRNHNSY-	-----	TLSNFNHSM	RITPKKSNNE	FRITAI	PCRG		79
Euplotes pep	KEVEEWKSL	-----	---GFAPCK	RLIPKKIT	FRIMTF	NKK		78
Trans of tetrahymen	KIQLEENLE	KVEEKLIPED	SFQKYPOCK	RUEPKKGS	FRIMTF	LRK		92
Consensus	K...E.....	-----F..CK	RITPKK	FRIMTF.RK		100
EST2 pep	ADEEBFTIYK	ENHKNAIQPT	QKILEYERNK	RPTSFTKIYS	PTQIADRIKE			129
Euplotes pep	IVNSDRKTTK	LTINTKLINS	HLMLKTEKN	-----RMFK	-DPFGFAVEN			120
Trans of tetrahymen	DKQKNIK---	LNLNQILMDS	QLVFRNLD	-----ML-G	-QKIGYSVFD			130
ConsensusK..K	LN.N..L..S	QL.L..EKN	-----	...IG..VF.			150
EST2 pep	FKQRLLEKN	NVL-----	EFVYFMKFD	VKSCYD				157
Euplotes pep	YD-DVMKAYE	EFVCKWKQVG	QKKEFFATMD	IEKCYD				155
Trans of tetrahymen	NK-QISEKFA	QFIEKWKNGK	REDEYYVTL	-----				158
Consensus	.K-...KKF.	.F..KWK..G	.E..YF.T.D	...CYD				186

[illegible]

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q .
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV

FIGURE 33

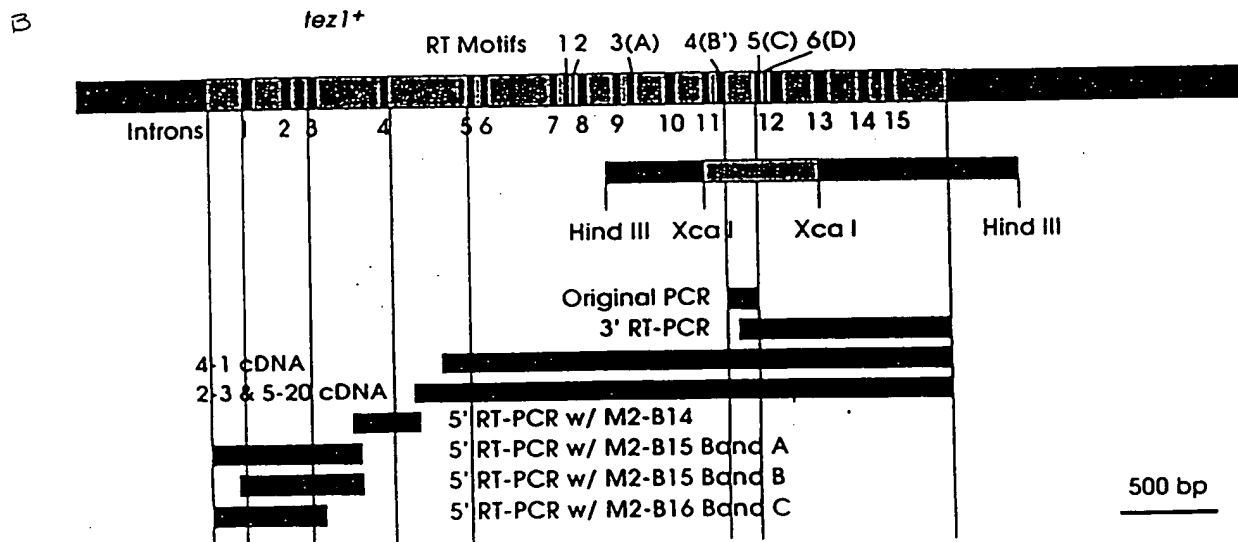
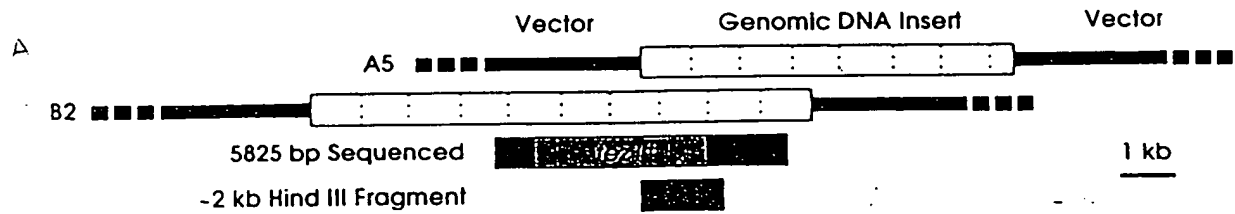


FIGURE 34

Poly 4

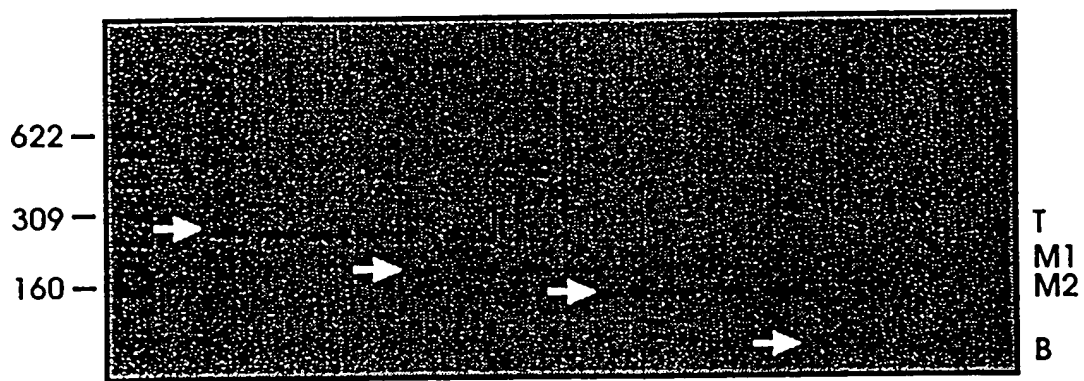
			t		t		c	
	t	a	a	g	c	c	t	c g
5'-	cag	acc	aaa	gga	att	cca	taa	gg -3'
	Q	T	K	G	I	P	Q	G

4 (B')

5 (c')

	D	D	Y	L	L	I	T	
3'-	ctg	ctg	atg	gag	gag	tag	tgg	-5'
	a	a	a	a	a	a	a	a
				t	t	t	t	
						c	c	
						<u>Poly 1</u>		

FIGURE 35



Motif B' (4)
QTKGIPQG

Motif C (5)
DDYLLIT

FIGURE 36

PCR Product M2 showed Reasonable Match with Other Telomerase Proteins

Ot	LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123	KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2	SILSSF LCHFYMEDLIDEYLSFTKKK-----GSVLLRVV
Sc_p103	DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS-----QDTLILKLADDFLIIS

. * . * . *

Q K V G I P Q G
caa aaa gtt ggt atc cct cag gg..... <---Actual Genomic Sequence.

Poly 4

t c
t a a g c c t c g
cag acc aaa gga att cca taa gg ---->

ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

K G I P S G S I L S S F L C H F Y M

GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E D L I D E Y L S F T K K K G S V L L R

GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg.

V V D D Y L L I T

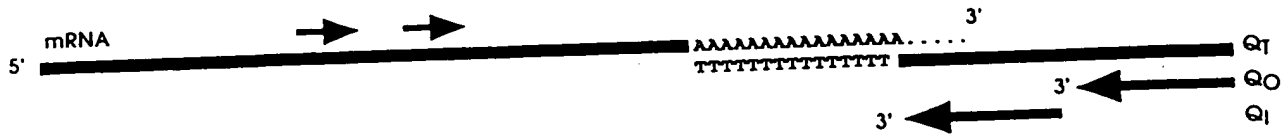
<---- ctg ctg atg gag gag tag tgg
a a a a a a a a
t t t t
c c

Poly 1

.....gac gat ttc ctc ttt ata aca..... <---Actual Genomic Sequence.
D D F L F I T

FIGURE 37

3' RT PCR Strategy



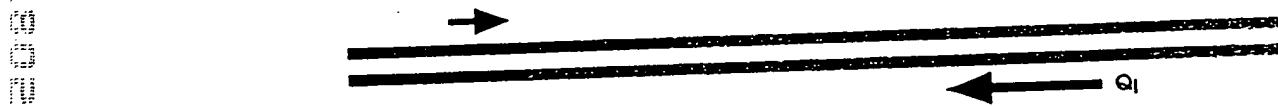
1. Synthesis of cDNA with Q_T Primer.



2. First Round PCR Using Outside Primer and Q_O Primer.



3. Second Round PCR Using Inside Primer and Q_I Primer.



4. Sequence Second Round PCR Products Using Inside Primer or Q_I Primer.



FIGURE 38

A

-Size Selected Libraries from P. Nurese

- 3 ~ 4 kb
- 5 ~ 6 kb
- 7 ~ 8 kb
- 11 ~ 12 kb

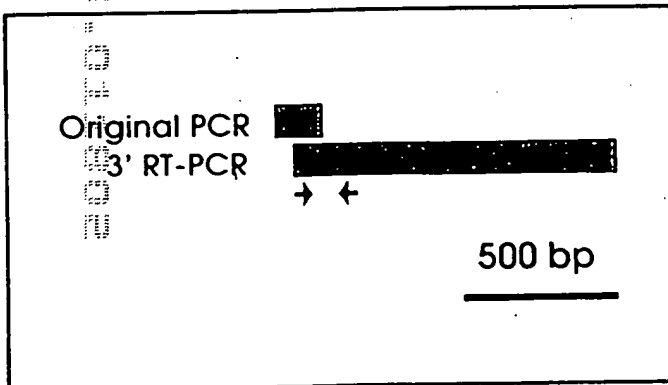
-Libraries from J.A. Wise

- Sau 3a Partial Digest
- Hind III Partial Digest

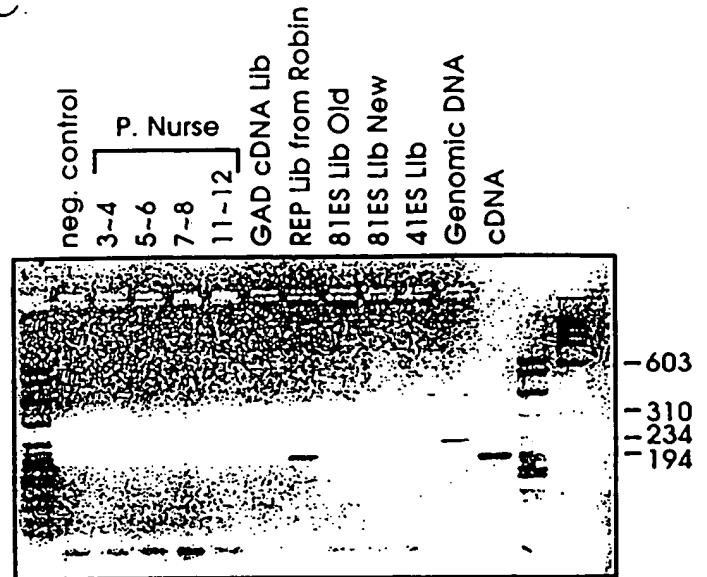
cDNA Libraries

- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

B.



C.



D.

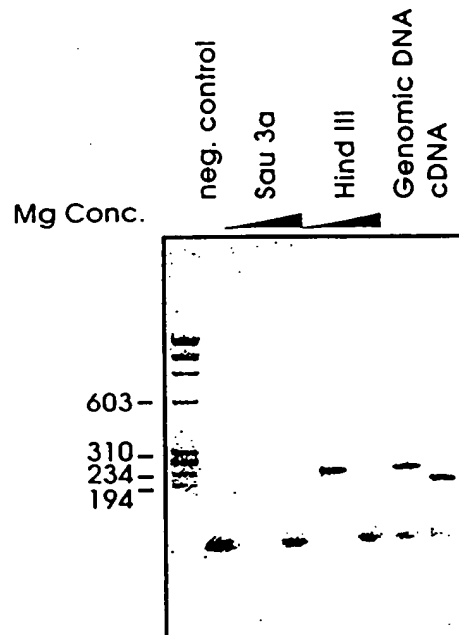
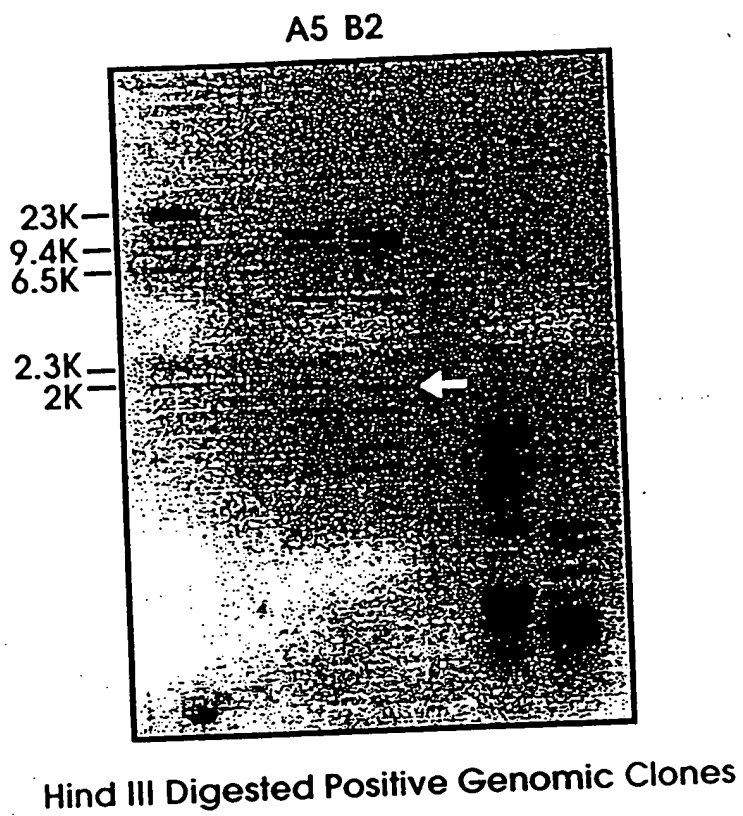
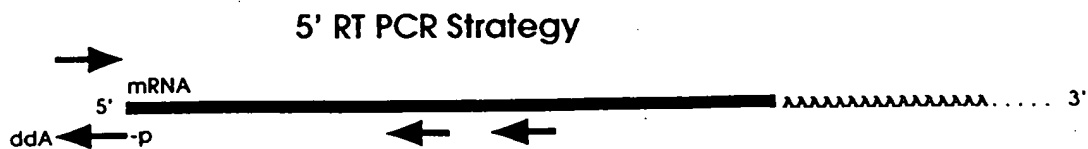


FIGURE 39

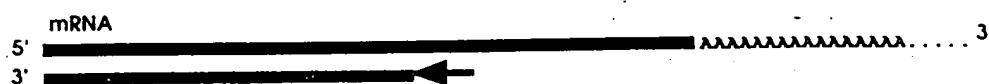


100541255 041800

FIGURE 40



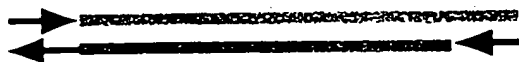
1. Synthesis of cDNA with Specific Downstream Primer.



2. Ligate Oligo with 5'-P and blocked 3' to cDNA using T4 RNA Ligase.



3. First Round PCR



4. Second Round PCR

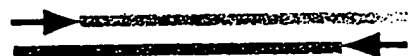


FIGURE 41

Alignment of RT Domains from Telomerase Catalytic Subunits.

		Motif O	
S.p.	Tez1p (429).	WLYNSFIIPILQSFYITESSDLRNRTVYFRKDIW ... (35)...	
S.c.	Est2p (366).	WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ... (35)...	
E.a.	p123 (441).	WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ... (35)...	
		* *** *	
		Motif 1 Motif 2 K	
		p hh h K hR h R	
S.p.	Tez1p	AVIRLLPKK--NTFRLITN-LRKRF ... (61)...	
S.c.	Est2p	SKMRIIPKKSNNFRIIAIPCRGAD ... (62)...	
E.a.	p123	GKLRLIPKK--TTFRPIMTFNKKIV ... (61)...	
		* *** * *	
		Motif 3(A) AF	
		h hDh GY h	
S.p.	Tez1p	KKYFVRIDIKSCYDRIKQDLMFRIVK ... (89)...	
S.c.	Est2p	ELYFMKFDVKSCYDSIPRMECMRILK ... (75)...	
E.a.	p123	KLFFATMDIEKCYDSVNREKLSTFLK ... (107)...	
		* * *** *	
		Motif 4(B')	
		hPQG pP hh h	
S.p.	Tez1p	YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ... (6)...	
S.c.	Est2p	YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ... (8)...	
E.a.	p123	YKQTKGIPQGLCVSSILSSFYYATLEESSLGF ... (14)...	
		* * ** * *	
		Y Motif 5(C) Motif 6(D)	
		h F DDhhh Gh h cK h	
S.p.	Tez1p	VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEEKHNFSTSLEKTVINFENS . (205)	
S.c.	Est2p	LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAPANRDKILAVSSQS . (173)	
E.a.	p123	LLMPLTDDYLLITTQENNAVLFIKLINVSRENGFKFNMKKLQTSFPLS . (209)	
		* * * * *	

FIGURE 42

A

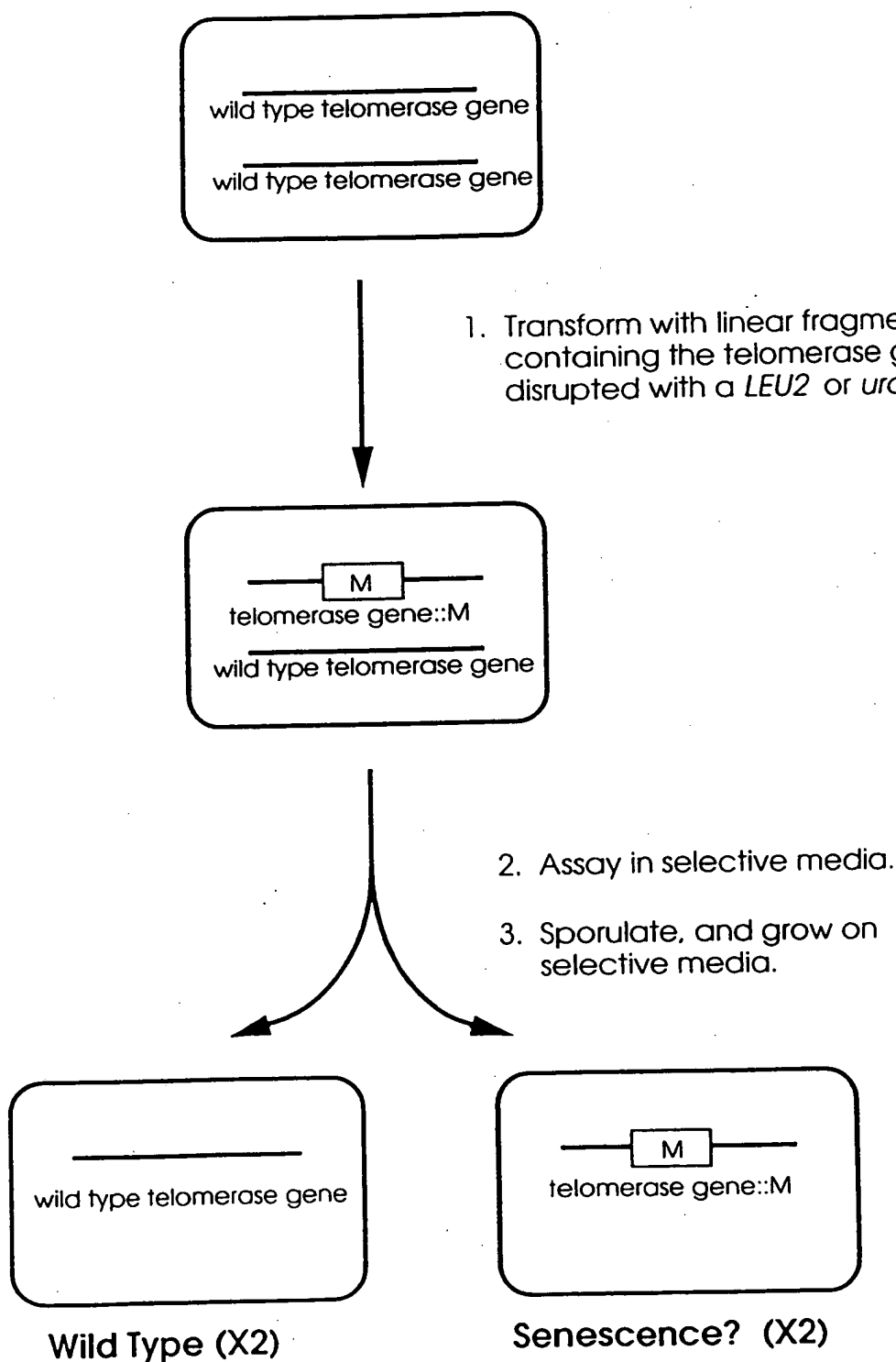
Sp_Tp1p :MTEHNTPKSRILRFLNCOYVYLCT
Sc_Ea2p :MKILFEF
Ea_p123 : MEVDVONQADHNGHNSALKYCEEIKKATLYSW
Sp_Tp1p : LNDYVOLYLRGSPA.....SHICERLRSDVOTFS
Sc_Ea2p : IODKLOIOLOTH.....ENLEKCGHNGOLD
Ea_p123 : IOKVIRCRNOSO.....DLEDIKIFAOTN
Sp_Tp1p : IFLNSTVVOFOSKPDQVOPSSPKCOSSELAN
Sc_Ea2p : ELITTCFALPNSKIALPCLPOLLSHKAYON
Ea_p123 : IVATPROYNEOSKVIARKEVFTOLMIELOK
Sp_Tp1p : VVKOMFDESERRA.....HLLM.....FSMNHEDFRAMH
Sc_Ea2p : CIIYLLTOELYN.....VLTVEKIHARNO
Ea_p123 : CLVELLSDDVSDROKLOCFOLKNGNO
Sp_Tp1p : VNGVQNDLYSTFPNLYSILESKHOLLLEI
Sc_Ea2p : VNNHLPCHSANSVNTLLKGAALKNFNSLV
Ea_p123 : LAKTHLTALSTOKOYFFOODNOVRAM
Sp_Tp1p : SDAMNYLSKOSIFEALPNOHYLSIPLFKH
Sc_Ea2p : TYAFVOLIHTYVIOFHGOFFYVKNCHPE
Ea_p123 : NELFNHTYKYLPORTSEOTLVPCNHYDM
Sp_Tp1p : NVFEET.....KRTIETSI.....SARKK
Sc_Ea2p : HLPK.....SSSSATAADI.....KOLTER
Ea_p123 : LKVNDFOKKOKOGAADMHEPCCSTCKYK
Sp_Tp1p : VNSISIRSFIFVSSSTKFOOLYFNHNSICD
Sc_Ea2p :KOFMKHINSSFFP
Ea_p123 : NEK.....DNFLNHNVPNWHNHSRTIIFYCTH
Sp_Tp1p : NTVHNMWLOWIFPROFOLINAFVOKHLEIPL
Sc_Ea2p :KILPSS.....SIKKLTOLREAF
Ea_p123 :NHOPKKEKNEFVSNNISAMDRQYI
Sp_Tp1p : VS.....OSTVVPKRLKYVPLIGOTAKRLHRIS
Sc_Ea2p : VS.....LVEIPORLKYVIMLTLOKLEKRLM
Ea_p123 : FTHIFRFRIRKELKOKVIEKIAVLEKVKDFN
Sp_Tp1p : LSKVYNNHYVIDTHODEKILSYLEKPHO
Sc_Ea2p : VYSILNHSIPLEGOTVLDKOSIPKLEK
Ea_p123 : FMYTLKSLPENWREKKEIENLINTREK
Sp_Tp1p :FAIRSVVVFVLI
Sc_Ea2p :SKYVEELFSTYTONKCTOHEFFYNI
Ea_p123 : VNOHIFEILIDETFKSRYSPSLNHYMS
Sc_Ea2p : FSKKOKHMLHLLVLPDOK
Ea_p123 : LTGRRKHFKEKVEYVEMKMLINKML
Sp_Tp1p : NIKISEILVLOKRSNAKCLSDPKKOIFA
Sc_Ea2p : KLRKDFLFI.....DIWFKHNFHNLOLA
Ea_p123 : KINTREIMOVETSAKHFVFDHNTVW
Sp_Tp1p : EFIVLYNSFIPILOS.....SSDLNHRV
Sc_Ea2p : CFISLFDOLIPKIIOTCISSTVTIV
Ea_p123 : KLLRIFEDLVSLIRC.....OOKSYSTY
Sp_Tp1p : FKDIKLLCPFFISMEKEAFKIHENNVAMD
Sc_Ea2p : VKHIDVIMKESADLKEETLAEVOEKVEE
Ea_p123 : TOKYTLPPAVIL.....NTLTHLRFL
Sc_Ea2p : VTLNHNHSD.....SHNHEIATPCROAD
Ea_p123 : KKLQAPAPGKLLI.....YTPNTFNKIV
Sp_Tp1p : IKMOSHEKMLVSTNOTLRPVASIKHIL
Sc_Ea2p : EEEPTITKEHNEKAIOTOKIETAKRPT
Ea_p123 : NSD.....KRTTELYTLLNHLMTKRMF
Sp_Tp1p : ESSDIPFNLKYLTKKOLLNRMFORKE
Sc_Ea2p : SPYKISPTOIAADRIKEPOLLKFMHVL
Ea_p123 : KDPPOFAYFHTODVMEKEEPCVWKOVOGKL
Sp_Tp1p : VYRIKESRIKODLNFRIYKKEDEP
Sc_Ea2p : VMKFVKSIPAMECHNILDALRENO
Ea_p123 : FMTATIEKSVNREKLSPLTYELLSSD
Sp_Tp1p : VIRKATINATSDRATEN
Sc_Ea2p : FVRSOYFFHTNG
Ea_p123 : WMTAOLKRNHNIVDSKPRKEMKDYPROK
Sp_Tp1p : FVSEAFSTYDMVFFERVOLL.....MKTSDFV
Sc_Ea2p :VLEKLFVNASR.....VPYPTI
Ea_p123 : FOKIALEGOOYPTLFLENEONDLNAKEIV
Sp_Tp1p : DEVOYNTESSEIFKMLKHLSONHVIKIONO
Sc_Ea2p : ONHTYLLHODVINYEMEIKTALWEDC
Ea_p123 : EAKORNYFKEDNLLPOINICOVYINPHOF
Sp_Tp1p : LKRV.....FCKHNEIDCSITK
Sc_Ea2p : IRED.....APIVOLYLFEKKA
Ea_p123 : KETKLCYINSSATISSOLR
Sp_Tp1p : KKO.....SVLLRYVFTVUNKDARK
Sc_Ea2p : SP3OD.....LILKLA.....STOQOYIN
Ea_p123 : DESMHPNPNVLLMLTYVITTOENHVL
Sp_Tp1p : FLNLSLROFKNHPSLCTVINFENNG
Sc_Ea2p : IKELANDOFKYNAKAMROILAYSSOD
Ea_p123 : FIEKLINVSRENOPFNNLOTSPLPSKFA
Sp_Tp1p :LINTFFESKKRPFVVRNSDYLL
Sc_Ea2p :ODTVIOFCA.....MHIFKEVWNSHTM
Ea_p123 : KYOMSYEEONIVODYCDWIGISOMKTLALMP
Sp_Tp1p : ACPKONALFNSTSVCTENHOKSFFIRNS
Sc_Ea2p : NFNHRSKSGOIFRSIALFNHISYTIOTN
Ea_p123 : INLRIGILCTNLHNMOTKASWMLKELF
Sp_Tp1p : AIAOPIIDFSCFMCHIVRGYCMUR
Sc_Ea2p : NHTNLMFROKIVYVNI
Ea_p123 : MNNHNYFRKITTEDFANKTLNKFISGOYK
Sp_Tp1p : AOA.....FORMFITOLLNVIORKWKK
Sc_Ea2p :KAPLS.....VTOMOFNSFLORIEH
Ea_p123 : YMOCAEYNNKKNLANSDILEVSKITSVY
Sp_Tp1p : LAEILGYTSRRFLSSAEVWFLCLOMROCKPS
Sc_Ea2p : TVSOCPITECDPLIEVVRFTILNDOLESS
Ea_p123 : TRAFFYLVCHIKOTIFQEEVPOFESTENF
Sp_Tp1p : FYNPPCFEOLIVOSLTDLIEPLRPYGOVLY
Sc_Ea2p : TS.....KONIKELIONDAYIT
Ea_p123 : IEIFS.....TEKVIHRYVCHLAKAKKSDOC
Sp_Tp1p : LNRRIAD
Sc_Ea2p : IYINVN
Ea_p123 : OSLIOYDA

B

Sp_Tp1p :MTEHNTPKSRILRFLNCOYVYLCT
Sc_Ea2p :MKILFEF
Ea_p123 : MEVDVONQADHNGHNSALKYCEEIKKATLYSW
Sp_Tp1p : LNDYVOLYLRGSPA.....SHICERLRSDVOTFS
Sc_Ea2p : IODKLOIOLOTH.....ENLEKCGHNGOLD
Ea_p123 : IOKVIRCRNOSO.....DLEDIKIFAOTN
Sp_Tp1p : IFLNSTVVOFOSKPDQVOPSSPKCOSSELAN
Sc_Ea2p : ELITTCFALPNSKIALPCLPOLLSHKAYON
Ea_p123 : IVATPROYNEOSKVIARKEVFTOLMIELOK
Sp_Tp1p : VVKOMFDESERRA.....HLLM.....FSMNHEDFRAMH
Sc_Ea2p : CIIYLLTOELYN.....VLTVEKIHARNO
Ea_p123 : CLVELLSDDVSDROKLOCFOLKNGNO
Sp_Tp1p : VNGVQNDLYSTFPNLYSILESKHOLLLEI
Sc_Ea2p : VNNHLPCHSANSVNTLLKGAALKNFNSLV
Ea_p123 : LAKTHLTALSTOKOYFFOODNOVRAM
Sp_Tp1p : SDAMNYLSKOSIFEALPNOHYLSIPLFKH
Sc_Ea2p : TYAFVOLIHTYVIOFHGOFFYVKNCHPE
Ea_p123 : NELFNHTYKYLPORTSEOTLVPCNHYDM
Sp_Tp1p : NVFEET.....KRTIETSI.....SARKK
Sc_Ea2p : HLPK.....SSSSATAADI.....KOLTER
Ea_p123 : LKVNDFOKKOKOGAADMHEPCCSTCKYK
Sp_Tp1p : VNSISIRSFIFVSSSTKFOOLYFNHNSICD
Sc_Ea2p :KOFMKHINSSFFP
Ea_p123 : NEK.....DNFLNHNVPNWHNHSRTIIFYCTH
Sp_Tp1p : NTVHNMWLOWIFPROFOLINAFVOKHLEIPL
Sc_Ea2p :KILPSS.....SIKKLTOLREAF
Ea_p123 :NHOPKKEKNEFVSNNISAMDRQYI
Sp_Tp1p : VS.....OSTVVPKRLKYVPLIGOTAKRLHRIS
Sc_Ea2p : VS.....LVEIPORLKYVIMLTLOKLEKRLM
Ea_p123 : FTHIFRFRIRKELKOKVIEKIAVLEKVKDFN
Sp_Tp1p : LSKVYNNHYVIDTHODEKILSYLEKPHO
Sc_Ea2p : VYSILNHSIPLEGOTVLDKOSIPKLEK
Ea_p123 : FMYTLKSLPENWREKKEIENLINTREK
Sp_Tp1p :FAIRSVVVFVLI
Sc_Ea2p :SKYVEELFSTYTONKCTOHEFFYNI
Ea_p123 : VNOHIFEILIDETFKSRYSPSLNHYMS
Sc_Ea2p : FSKKOKHMLHLLVLPDOK
Ea_p123 : LTGRRKHFKEKVEYVEMKMLINKML
Sp_Tp1p : NIKISEILVLOKRSNAKCLSDPKKOIFA
Sc_Ea2p : KLRKDFLFI.....DIWFKHNFHNLOLA
Ea_p123 : KINTREIMOVETSAKHFVFDHNTVW
Sp_Tp1p : EFIVLYNSFIPILOS.....SSDLNHRV
Sc_Ea2p : CFISLFDOLIPKIIOTCISSTVTIV
Ea_p123 : KLLRIFEDLVSLIRC.....OOKSYSTY
Sp_Tp1p : FKDIKLLCPFFISMEKEAFKIHENNVAMD
Sc_Ea2p : VKHIDVIMKESADLKEETLAEVOEKVEE
Ea_p123 : TOKYTLPPAVIL.....NTLTHLRFL
Sc_Ea2p : VTLNHNHSD.....SHNHEIATPCROAD
Ea_p123 : KKLQAPAPGKLLI.....YTPNTFNKIV
Sp_Tp1p : IKMOSHEKMLVSTNOTLRPVASIKHIL
Sc_Ea2p : EEEPTITKEHNEKAIOTOKIETAKRPT
Ea_p123 : NSD.....KRTTELYTLLNHLMTKRMF
Sp_Tp1p : ESSDIPFNLKYLTKKOLLNRMFORKE
Sc_Ea2p : SPYKISPTOIAADRIKEPOLLKFMHVL
Ea_p123 : KDPPOFAYFHTODVMEKEEPCVWKOVOGKL
Sp_Tp1p : VYRIKESRIKODLNFRIYKKEDEP
Sc_Ea2p : VMKFVKSIPAMECHNILDALRENO
Ea_p123 : FMTATIEKSVNREKLSPLTYELLSSD
Sp_Tp1p : VIRKATINATSDRATEN
Sc_Ea2p : FVRSOYFFHTNG
Ea_p123 : WMTAOLKRNHNIVDSKPRKEMKDYPROK
Sp_Tp1p : FVSEAFSTYDMVFFERVOLL.....MKTSDFV
Sc_Ea2p :VLEKLFVNASR.....VPYPTI
Ea_p123 : FOKIALEGOOYPTLFLENEONDLNAKEIV
Sp_Tp1p : DEVOYNTESSEIFKMLKHLSONHVIKIONO
Sc_Ea2p : ONHTYLLHODVINYEMEIKTALWEDC
Ea_p123 : EAKORNYFKEDNLLPOINICOVYINPHOF
Sp_Tp1p : LKRV.....FCKHNEIDCSITK
Sc_Ea2p : IRED.....APIVOLYLFEKKA
Ea_p123 : KETKLCYINSSATISSOLR
Sp_Tp1p : KKO.....SVLLRYVFTVUNKDARK
Sc_Ea2p : SP3OD.....LILKLA.....STOQOYIN
Ea_p123 : DESMHPNPNVLLMLTYVITTOENHVL
Sp_Tp1p : FLNLSLROFKNHPSLCTVINFENNG
Sc_Ea2p : IKELANDOFKYNAKAMROILAYSSOD
Ea_p123 : FIEKLINVSRENOPFNNLOTSPLPSKFA
Sp_Tp1p :LINTFFESKKRPFVVRNSDYLL
Sc_Ea2p :ODTVIOFCA.....MHIFKEVWNSHTM
Ea_p123 : KYOMSYEEONIVODYCDWIGISOMKTLALMP
Sp_Tp1p : ACPKONALFNSTSVCTENHOKSFFIRNS
Sc_Ea2p : NFNHRSKSGOIFRSIALFNHISYTIOTN
Ea_p123 : INLRIGILCTNLHNMOTKASWMLKELF
Sp_Tp1p : AIAOPIIDFSCFMCHIVRGYCMUR
Sc_Ea2p : NHTNLMFROKIVYVNI
Ea_p123 : MNNHNYFRKITTEDFANKTLNKFISGOYK
Sp_Tp1p : AOA.....FORMFITOLLNVIORKWKK
Sc_Ea2p :KAPLS.....VTOMOFNSFLORIEH
Ea_p123 : YMOCAEYNNKKNLANSDILEVSKITSVY
Sp_Tp1p : LAEILGYTSRRFLSSAEVWFLCLOMROCKPS
Sc_Ea2p : TVSOCPITECDPLIEVVRFTILNDOLESS
Ea_p123 : TRAFFYLVCHIKOTIFQEEVPOFESTENF
Sp_Tp1p : FYNPPCFEOLIVOSLTDLIEPLRPYGOVLY
Sc_Ea2p : TS.....KONIKELIONDAYIT
Ea_p123 : IEIFS.....TEKVIHRYVCHLAKAKKSDOC
Sp_Tp1p : LNRRIAD
Sc_Ea2p : IYINVN
Ea_p123 : OSLIOYDA

FIGURE 43

Disruption strategy for the putative telomerase genes.



(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIGURE 44

An Example of Confirmation of *tez1* disruption By PCR

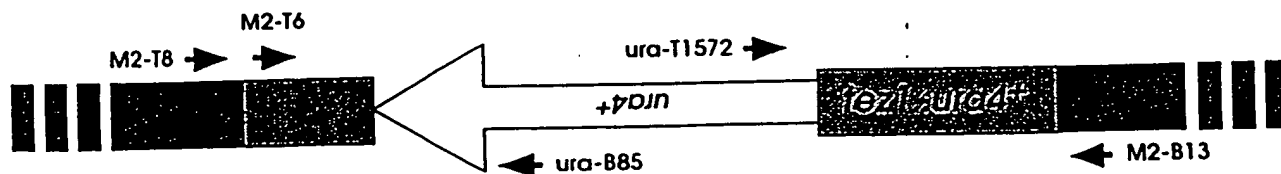
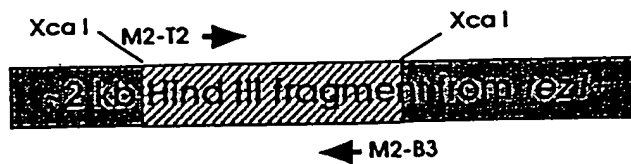
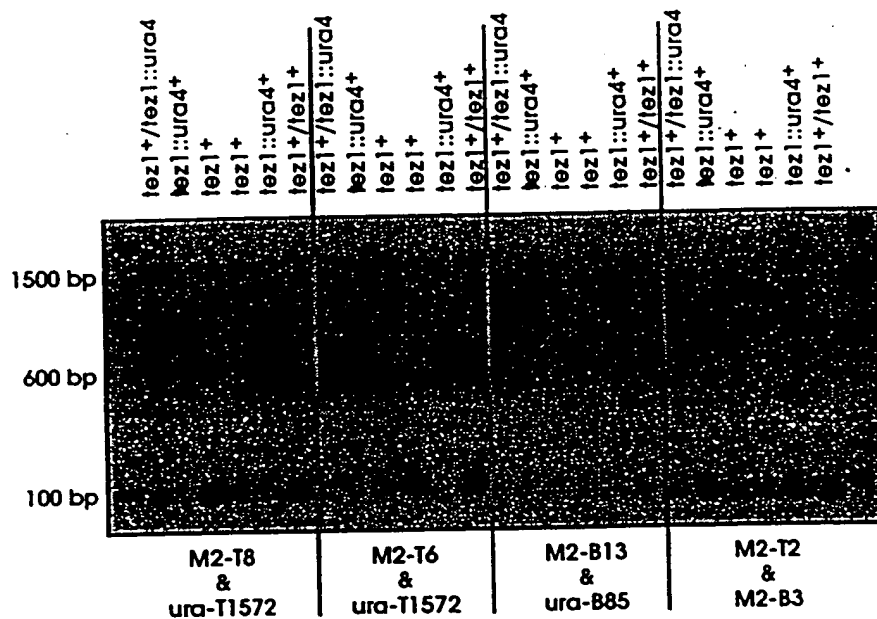


FIGURE 45

Tez1 disruption causes progressive shortening of telomeres in *S. pombe*

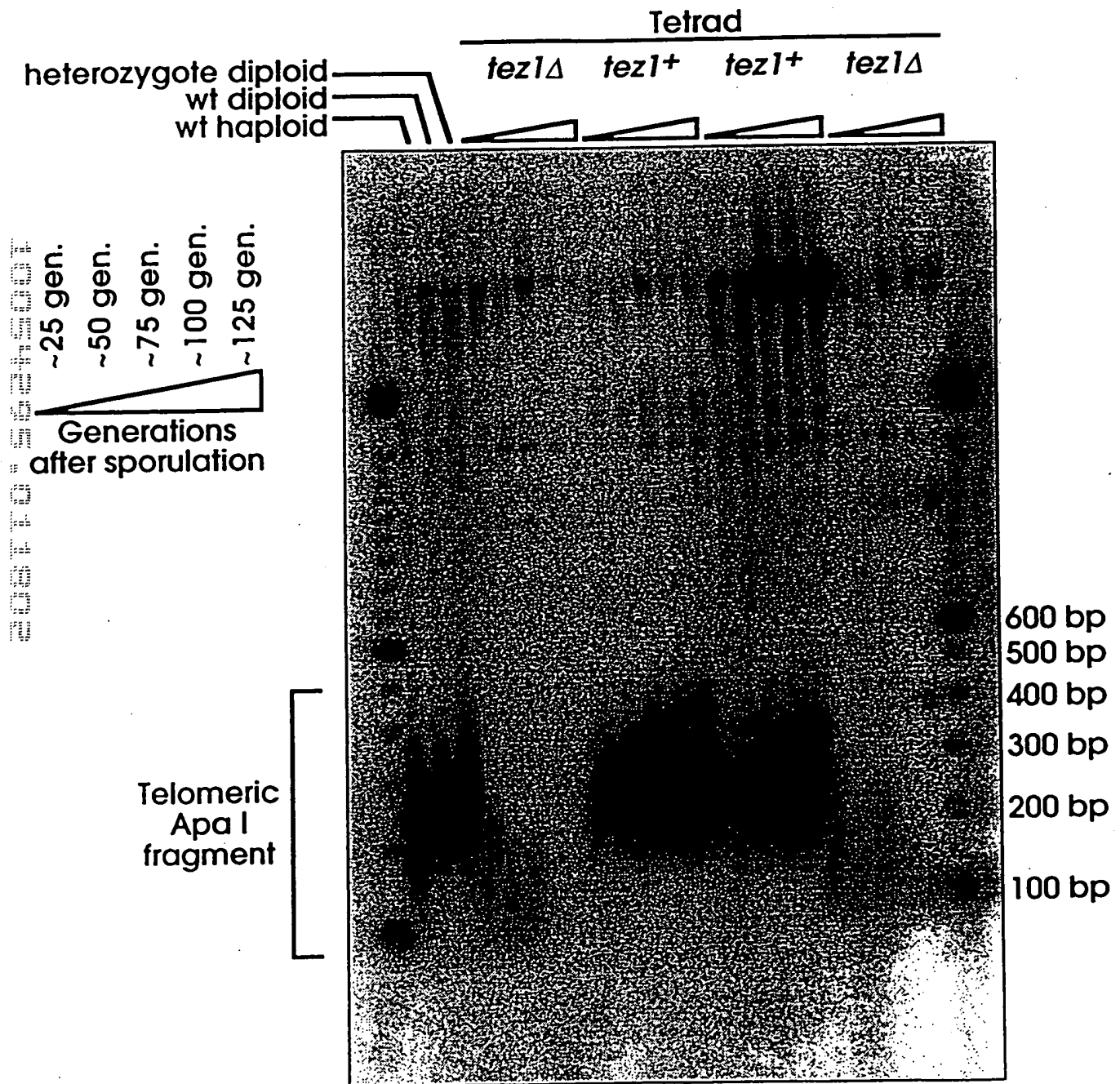


FIGURE 46

1 ggtaccgatttacttttctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga 80
 81 actcaataacaataccaagtcaaattccaatatgaagggtgttatttagtgatcgataaatatttctattttatcgggtcgta 160
 161 ccaagtataaggacaaaaagaacaacttcttccccctaaagacttttactttattaatttacttttcaaataatatttcg 240
 241 ggttcgcttacttttaacgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgatcattggatat 320
 321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtcggtgcatattc 400
 401 ttaacatggagccttacacttttagatgagtcacgtcgcgatgatggagtatttgggtatcatccaacgtttgccttgaaaag 480
 481 gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagttttttgatgcttgacacgtctagcatg 560
 561 attgagatattcaaaaatttctatccactacaactcctttaacgcggtttttatttttctattttctatttctcatgttggt 640
 641 ccaaatatgtatcatctcgtattaggttttttccggttttactcctggaatcgtacctttttcactattccccctaataga 720
 721 ataactctaaattagtttctgcttataattgatagtagtagaaaagattgggtgattctactcgtgtaatgttattagtttaaa 800
 801 gatacttttgcaaaacattttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
 881 actattttatttaaaacggttatgatcagtaggacactttgcataatatatagttatgcttaatgggttacttgtaacttgc 958

 959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
 1 M T E H H T P K S R I L R F L E N Q Y V 20
 1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
 21 Y L C T L N D Y V Q L V L R G S P A S S 40
 1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
 41 Y S N I C E R L R S D V Q T S F S I F L 60
 1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
 61 H S T V V G F D S K P D E G V Q F S S P 80

FIGURE 46 (cont.)

1199	AAA	TGC	TCA	CAG	TCA	GAG	gtatatatatatttttgttttgatttttttctattcgggatagctaatatatgggcag	1272
81	K	C	S	Q	S	E		86
1273	CTA	ATA	GCG	AAT	GTT	GTA	AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA	1332
87	L	I	A	N	V	V	K Q M F D E S F E R R R N L	106
1333	CTG	ATG	AAA	GGG	TTT	TCC	ATG gtaaggtatttctaattgtgaaatatttacctgcaattactgtttcaaagaga	1405
107	L	M	K	G	F	S	M	113
1406	ttgtattttaaccgataaag	AAT	CAT	GAA	GAT	TTT	CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT	1469
114		N	H	E	D	F	R A M H V N G V Q N	128
1470	GAT	CTC	GTT	TCT	ACT	TTT	CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA	1529
129	D	L	V	S	T	F	P N Y L I S I L E S K N W Q	148
1530	CTT	TTG	TTA	GAA	AT	gtaaataccgggtaagatggttgcgacactttgaacaagactgacaagtatag	T ATC GGC	1601
149	L	L	L	E	I		I G	155
1602	AGT	GAT	GCC	ATG	CAT	TAC	TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC	1661
156	S	D	A	M	H	Y	L L S K G S I F E A L P N D	175
1662	AAT	TAC	CTT	CAG	ATT	TCT	GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG	1721
176	N	Y	L	Q	I	S	G I P L F K N N V F E E T V	195
1722	TCA	AAA	AAA	AGA	AAG	CGA	ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA	1781
196	S	K	K	R	K	R	T I E T S I T Q N K S A R K	215
1782	GAA	GTT	TCC	TGG	AAT	AGC	ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT	1841
216	E	V	S	W	N	S	I S I S R F S I F Y R S S Y	235
1842	AAG	AAG	TTT	AAG	CAA	G	gtaactaataactggttatccttcataactaatttttag	AT CTA TAT TTT AAC
1907								
236	K	K	F	K	Q	D		L Y F N 245
1908	TTA	CAC	TCT	ATT	TGT	GAT	CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG	1967
246	L	H	S	I	C	D	R N T V H M W L Q W I F P R	265
1968	CAA	TTT	GGA	CTT	ATA	AAC	GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA	2027
266	Q	F	G	L	I	N	A F Q V K Q L H K V I P L V	285
2028	TCA	CAG	AGT	ACA	GTT	GTG	CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA	2087
286	S	Q	S	T	V	V	P K R L L K V Y P L I E Q T	305
2088	GCA	AAG	CGA	CTC	CAT	CGT	ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT	2147
306	A	K	R	L	H	R	I S L S K V Y N H Y C P Y I	325
2148	GAC	ACC	CAC	GAT	GAT	GAA	AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG	2207
326	D	T	H	D	D	E	K I L S Y S L K P N Q V F A	345
2208	TTT	CTT	CGA	TCC	ATT	CTT	GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA	2267
346	F	L	R	S	I	L	V R V F P K L I W G N Q R I	365
2268	TTT	GAG	ATA	ATA	TTA	AAA	G gtattgtataaaaattttattaccactaacgattttaccag	AC CTC GAA ACT 2336
366	F	E	I	I	L	K	D	L E T 375

FIGURE 46 (cont.)

2337	TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG	2396
376	F L K L S R Y E S F S L H Y L M S N I K	395
2397	gtaatatgccaaatttttttaccattaattaacaatcag	2465
396	I S E I E W L V L G	405
2466	AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG	2525
406	K R S N A K M C L S D F E K R K Q I F A	425
2526	GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT	2585
426	E F I Y W L Y N S F I I P I L Q S F F Y	445
2586	ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA	2645
446	I T E S S D L R N R T V Y F R K D I W K	465
2646	CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA-ATA AAC GAG	2705
466	L L C R P F I T S M K M E A F E K I N E	485
2706	gtatttttaaagtattttttgcaaaaagctaatttttcag	2775
486	N N V R M D T Q K T	495
2776	ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG	2835
496	T L P P A V I R L L P K K N T F R L I T	515
2836	AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaatttttgggtcatcaatgtactttacttctaattctatta	2906
516	N L R K R F L I K	524
2907	ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG	2967
525	M G S N K K M L V S T N Q T L R P V	542
2968	GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG	3027
543	A S I L K H L I N E E S S G I P F N L E	562
3028	GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat	3088
563	V Y M K L L T F K K D L L K H R M F G	581
3089	tatataatgcgcgattcctcattattaattttgcag	3155
582	R K K Y F V R I D I	591
3156	AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC	3215
592	K S C Y D R I K Q D L M F R I V K K K L	611
3216	AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT	3275
612	K D P E F V I R K Y A T I H A T S D R A	631
3276	ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttattttttcattggaattttttaacaa	3343
632	T K N F V S E A F S Y F	643
3344	attcttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA	3405
644	D M V P F E K V V Q L L S M K T	659
3406	TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT	3465
660	S D T L F V D F V D Y W T K S S S E I F	679
3466	AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca	3532
680	K M L K E H L S G H I V K	692

FIGURE 46 (cont.)

3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593
693 I G N S Q Y L Q K V G I P Q G S 708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653
709 I L S S F L C H F Y M E D L I D E Y L S 728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713
729 F T K K K G S V L L R V V D D F L F I T 748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgtcattcc 3777
749 V N K K D A K K F L N L S L R G 764

3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840
765 F E K H N F S T S L E K T V 778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA 3900
779 I N F E N S N G I I N N T F F N E S K K 798

3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
799 R M P F F G F S V N M R S L D T L L A C 818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
819 P K I D E A L F N S T S V E L T K H M G 838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
839 K S F F Y K I L R S 848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
849 S L A S F A Q V F I D I T H N S K F N S 868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
869 C C N I Y R L G Y S M C M R A Q A Y L K 888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
889 R M K D I F I P Q R M F I T D 903

4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
904 L L N V I G R K I W K K L A 917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
918 E I L G Y T S R R F L S S A E V K W 935

4402 ggtctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468
936 L F C L G M R D G L K 946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
947 P S F K Y H P C F E Q L I Y Q F Q S L T 966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA 4588
967 D L I K P L R P V L R Q V L F L H R R I 986

4589 GCT GAT TAA tgtcattttcaattttattatatacatcctttattactggtgtcttaacaatattattactaagtata 4665
987 A D * 989

FIGURE 46 (cont.)

[illegible]

FIGURE 47

1
GCCAAGTTCCTGCACTGGCTG met ser val tyr val val glu leu leu
ATG AGT GTG TAC GTC GTC GAG CTG CTC

10 20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

40 50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

70 80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

100 110
glu lys ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130 140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

160 170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

FIGURE 47 (cont.)

190 thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG

200

210 gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220 gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

230

240 leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250 arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

260

270 thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280 arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

290

300 val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310 phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

320

330 leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340 tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

350

360 phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370 arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

380

FIGURE 47 (cont.)

390
 leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
 CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

 400 410
 ala tyr arg phe his ala cys val leu gln leu pro phe his gln
 GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

 420
 gln val trp lys asn pro his phe ser cys ala ser ser leu thr
 CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

 430 440
 arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
 CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

 450
 val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
 GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

 460 470
 arg ala val ala val pro pro ser ile pro ala gln ala asp ser
 CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

 480
 thr pro cys his leu arg ala thr pro gly val thr gln asp ser
 ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

 490 500
 pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
 CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

 510
 pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
 CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

 520 530
 his pro gly leu met ala thr arg pro gln pro gly arg glu gln
 CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

 540
 thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
 ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

 550 560
 arg gly gly pro his pro gly leu his arg trp glu ser glu ala
 AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

 564
 OP
 TGA GTGAGTGT TTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC

 CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

FIGURE 47 (cont.)

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT
CCCCACATAGGAATAGTCCATCCCCAGATTGCGCATTTGTTACCCCTTCGCCCTGCCTTCC
TTTGCCTTCCACCCCCACCATTTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG
AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG
GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT
TTTCAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 48

Motif -1
 Ep p123 ...LVVSLIRCFYVTEQQKSYSKT...
 Sp Tez1 ...FIIPILQSFFYITESSDLNRNT...
 Sc Est2 ...LIPKIIQTFFYCTEISSTVTIV...
 Hs TCP1 ...YVVELLRSEFFYVTETTFQKNRL...
 consensus FFY TE

Motif 0
 Ep p123 ...KSLGFAPGKRLRLIPKKT--TFRPIMTFNKKIV...
 Sp Tez1 ...QKTTLPAPVIRLLPKKN--TFRLLITNLRKRFL...
 Sc Est2 ...TLNFNHSHKMRIPKKSNNEFRIIAIPCRGAD...
 Hs TCP1 ...ARPAALLTSRLRFIPKPD--GLRPIVNMDYVVG...
 consensus R PK RI

Motif A
 Ep p123 ...PKLFFATMDIEKCYDSVNREKLSTFLK...
 Sp Tez1 ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
 Sc Est2 ...PELYFMKFDVKSCYDSIPRMECMRILK...
 Hs TCP1 ...PELYFVKVDVTGAYDTIPQDRLTEVIA...//...
 consensus F D YD

Motif B
 Ep p123 ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
 Sp Tez1 ...GNSQYLQKVGIPQGSILSSFLCHFYME...
 Sc Est2 ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
 Hs TCP1 ...RATSYVQCQGIPQGSILSTLLCSLCYG...
 consensus G QG S

Motif C
 Ep p123 ...PNVNLLMRLTDDYLLITTQENN...
 Sp Tez1 ...KKGSVLLRVVDDFLFITVNKKD...
 Sc Est2 ...SQDTLILKLADDFLIISTDQQQ...
 Hs TCP1 ...RRDGLLLRLVDDFLLVTPHLTH...
 consensus DD L

Motif D
 Ep p123 ...NVSRENGFKFNMKKL...
 Sp Tez1 ...LNLSLRGFEEKHNFST...
 Sc Est2 ...KKLAMGGFQKYNKA...
 Hs TCP1 ...LRTLVRGVPEYGCVV...
 consensus G

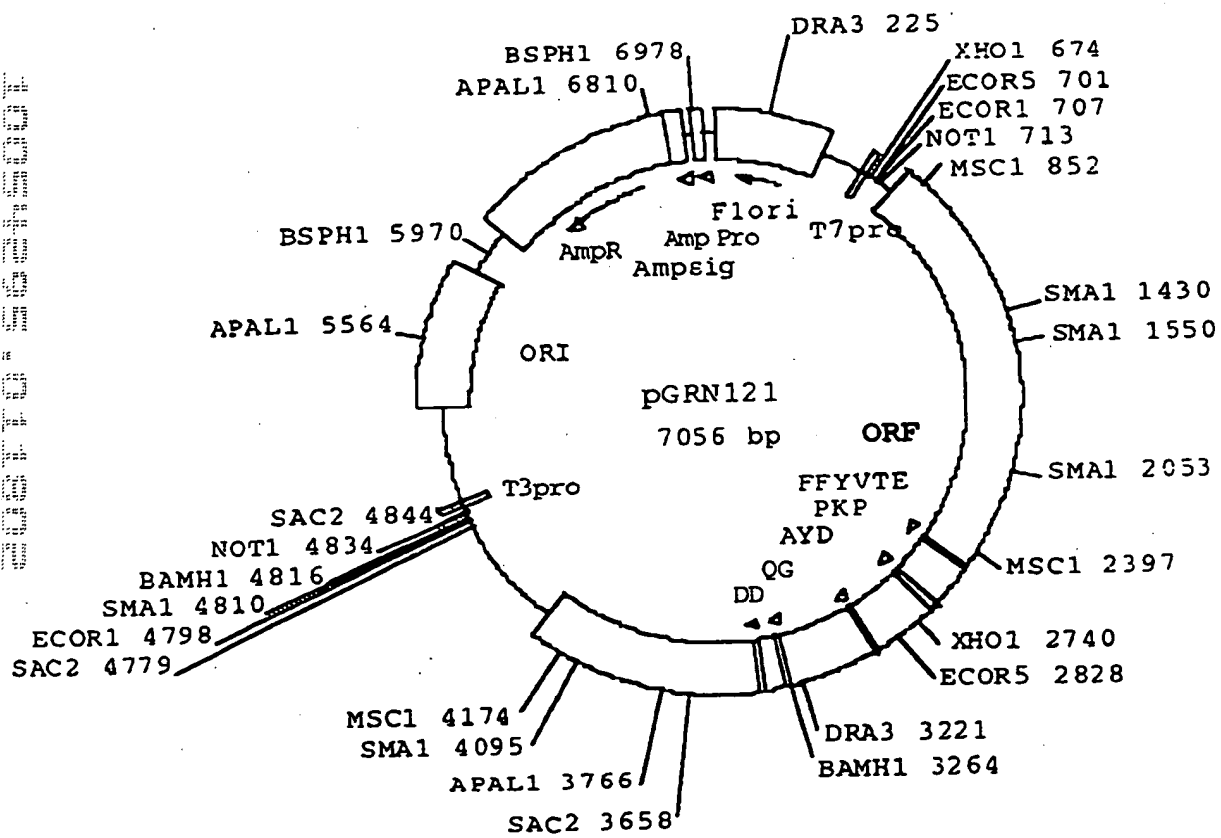
[illegible]

FIGURE 50

1 GCAGCGCTGC GTCCTGCTGC GCACGTGGGA AGCCCTGGCC CCGGCCACCC
 51 CCGCGATGCC GCGCGCTCCC CGCTGCCGAG CCGTGCGCTC CCTGCTGCGC
 101 AGCCACTACC GCGAGGTGCT GCCGCTGGCC ACGTTCGTGC GGCGCCTGGG
 151 GCCCCAGGGC TGGCGGCTGG TGCAGCGCGG GGACCCGGCG GCTTTCGCG
 201 CGNTGGTGGC CCANTGCNTG GTGTGCGTGC CCTGGGANGN ANGGCNGCCC
 251 CCCGCCGCCC CCTCCTCCG CCAGGTGTCC TGCCTGAANG ANCTGGTGGC
 301 CCGAGTGCTG CANANGCTGT GCGANCGCGG CGCGAANAAC GTGCTGGCCT
 351 TCGGCTTCGC GCTGCTGGAC GGGGCCCGCG GGGGCCCCC CGAGGCCTTC
 401 ACCACCAGCG TGCGCAGCTA CCTGCCCAAC ACGGTGACCG ACGCACTGCG
 451 GGGGAGCGGG GCGTGGGGGC TGCTGCTGCG CCGCGTGGG GACGACGTGC
 501 TGGTTCACCT GCTGGCACGC TGC CGCNTNT TTGTGCTGGT GGNTCCCAGC
 551 TGCGCCTACC ANGTGTGCGG GCCGCCGCTG TACCAGCTCG GCGCTGCNAC
 601 TCAGGCCCGG CCCCCGCCAC ACGCTANTGG ACCCGAANGC GTCTGGGATC
 651 CAACGGGCCT GGAACCATAG CGTCAGGGAG GCCGGGGTCC CCCTGGGCTG
 701 CCAGCCCCGG GTGCGAGGAG GCGCGGGGGC AGTGCCAGCC GAAGTCTGCC
 751 GTTGCCCAAG AGGCCAGGC GTGGCGCTGC CCCTGAGCCG GAGCGGACGC
 801 CCGTTGGGCA GGGGTCCTGG GCCACCCGG GCAGGACGCC TGGACCGAGT
 851 GACCGTGGTT TCTGTGTGGT GTCACCTGCC AGACCCGCCG AAGAAGCCAC
 901 CTCTTTGGAG GGTGCGCTCT CTGGCACGCG CCACTCCAC CCATCCGTGG
 951 GCCGCCAGCA CCACGCGGGC CCCCCATCCA CATCGCGGCC ACCACGTCCT
 1001 GGGACACGCC TTGTCCCCCG GTGTACGCCG AGACCAAGCA CTTCTCTAC
 1051 TCCTCAGGCG ACAAGNACAC TCGNCCCTC CTTCTACTC AATATATCTG
 1101 AGGCCAGCC TGA CTGGCGT TCGGGAGGTT CGTGGAGACA NTCTTTCTGG
 1151 TTCCAGGCCT TGGATGCCAG GATTCCCCG AGGTTGCCCC GCCTGCCCCA
 1201 GCGNTACTGG CAAATGCGGC CCCTGTTTCT GGAGCTGCTT GGGAACCAGC
 1251 CGCAGTGCCC CTACGGGGTG TTCCTCAAGA CGCACTGCCC GCTGCGAGCT
 1301 GCGGTCACCC CAGCAGCCGG TGTCTGTGCC CGGGAGAAGC CCCAGGGCTC
 1351 TGTGGCGGCC CCGAGGAGG AGGAACACAG ACCCCGTCG CCTGGTGCAG
 1401 CTGCTCCGCC AGCACAGCAG CCCCTGGCAG GTGTACGGCT TCGTGCGGGC
 1451 CTGCCTGCGC CGGCTGGTGC CCCCAGGCCT CTGGGGCTCC AGGCACAACG
 1501 AACGCCGCTT CCTCAGGAAC ACCAAGAAGT TCATCTCCCT GGGGAAGCAT
 1551 GCCAAGCTCT CGCTGCAGGA GCTGACGTGG AAGATGAGCG TGCGGGACTG
 1601 CGCTTGGCTG CGCAGGAGCC CAGGGGTTGG CTGTGTTCCG GCCGCAGAGC
 1651 ACCGTCTGCG TGAGGAGATC CTGGCCAAGT TCCTGCACTG GCTGATGAGT
 1701 GTGTACGTCG TCGAGCTGCT CAGGTCTTTC TTTTATGTCA CGGAGACCAC
 1751 GTTTCAAAAG AACAGGCTCT TTTTCTACCG GAAGAGTGTG TGGAGCAAGT
 1801 TGCAAAGCAT TGAATCAGA CAGCACTTGA AGAGGGTGCA GCTGCGGGAG
 1851 CTGTCGGAAG CAGAGGTCAG GCAGCATCGG GAAGCCAGGC CCGCCCTGCT
 1901 GACGTCCAGA CTCCGCTTCA TCCCCAAGCC TGACGGGCTG CGGCCGATTG
 1951 TGAACATGGA CTACGTCGTG GGAGCCAGAA CGTTCGCGAG AGAAAAGAGG
 2001 GCCGAGCGTC TCACCTCGAG GGTGAAGGCA CTGTTACGCG TGCTCAACTA
 2051 CGAGCGGGCG CGGCGCCCCG GCCTCCTGGG CGCCTCTGTG CTGGGCCTGG
 2101 ACGATATCCA CAGGGCCTGG CGCACCTTCG TGCTGCGTGT GCGGGCCAG
 2151 GACCCGCCGC CTGAGCTGTA CTTTGTCAAG GTGGATGTGA CGGGCGCGTA
 2201 CGACACCATC CCCCAGGACA GGCTCACGGA GGTCATCGCC AGCATCATCA
 2251 AACCCAGAA CACGTACTGC GTGCGTCGGT ATGCCGTGGT CCAGAAGGCC

FIGURE 50 (cont.)

2301 GCCCATGGGC ACGTCCGCAA GGCCTTCAAG AGCCACGTCT CTACCTTGAC
 2351 AGACCTCCAG CCGTACATGC GACAGTTCGT GGCTCACCTG CAGGANAACA
 2401 GCCCGCTGAG GGATGCCGTC GTCATCGAGC AGAGCTCCTC CCTGAATGAG
 2451 GCCAGCAGTG GCCTCTTCGA CGTCTTCCTA CGCTTCATGT GCCACCACGC
 2501 CGTGCGCATC AGGGGCAAGT CCTACGTCCA GTGCCAGGGG ATCCCGCAGG
 2551 GCTCCATCCT CTCCACGCTG CTCTGCAGCC TGTGCTACGG CGACATGGAG
 2601 AACAAGCTGT TTGCGGGGAT TCGGCGGGAC GGGCTGCTCC TGC GTTTGGT
 2651 GGATGATTTC TTGTTGGTGA CACCTCACCT CACCCACGCG AAAACCTTCC
 2701 TCAGGACCCT GGTCCGAGGT GTCCCTGAGT ATGGCTGCGT GGTGAACTTG
 2751 CGGAAGACAG TGGTGAACCT CCCTGTAGAA GACGAGGCCC TGGGTGGCAC
 2801 GGCTTTTGT CAGATGCCGG CCCACGGCCT ATTCCCCTGG TCGGCGCTGC
 2851 TGCTGGATAC CCGGACCCTG GAGGTGCAGA GCGACTACTC CAGCTATGCC
 2901 CGGACCTCCA TCAGAGCCAG TCTCACCTTC AACCGCGGCT TCAAGGCTGG
 2951 GAGGAACATG CGTCGCAAAC TCTTTGGGGT CTTGCGGGCTG AAGTGTACAC
 3001 GCCTGTTTCT GGATTTGCAG GTGAACAGCC TCCAGACGGT GTGCACCAAC
 3051 ATCTACAAGA TCCTCCTGCT GCAGGCGTAC AGGTTTCACG CATGTGTGCT
 3101 GCAGCTCCCA TTTCATCAGC AAGTTTGGAA GAACCCCAACA TTTTCTCTGC
 3151 GCGTCATCTC TGACACGGCC TCCCTCTGCT ACTCCATCCT GAAAGCCAAG
 3201 AACGCAGGGA TGTCGCTGGG GGCCAAGGGC GCCGCCGGCC CTCTGCCCTC
 3251 CGAGGCCGTG CAGTGGCTGT GCCACCAAGC ATTCCTGCTC AAGCTGACTC
 3301 GACACCGTGT CACCTACGTG CCACTCCTGG GGTCCTCAG GACAGCCCAG
 3351 ACGCAGCTGA GTCGGAAGCT CCCGGGGACG ACGCTGACTG CCCTGGAGGC
 3401 CGCAGCCAAC CCGGCACTGC CCTCAGACTT CAAGACCATC CTGGACTGAT
 3451 GGCCACCCGC CCACAGCCAG GCCGAGAGCA GACACCAGCA GCCCTGTCAC
 3501 GCCGGGCTCT ACGTCCCAGG GAGGGAGGGG CGGCCACAC CCAGGCCCGC
 3551 ACCGCTGGGA GTCTGAGGCC TGAGTGAGTG TTTGGCCGAG GCCTGCATGT
 3601 CCGGCTGAAG GCTGAGTGTG CGGCTGAGGC CTGAGCGAGT GTCCAGCCAA
 3651 GGGCTGAGTG TCCAGCACAC CTGCCGTCTT CACTTCCCA CAGGCTGGCG
 3701 CTCGGCTCCA CCCAGGGCC AGCTTTTCTT CACCAGGAGC CCGGCTTCCA
 3751 CTCCCCACAT AGGAATAGTC CATCCCCAGA TTCGCCATTG TTCACCCCTC
 3801 GCCCTGCCCT CCTTTGCCTT CCACCCCCAC CATCCAGGTG GAGACCCTGA
 3851 GAAGGACCCT GGGAGCTCTG GGAATTTGGA GTGACCAAAG GTGTGCCCTG
 3901 TACACAGGCG AGGACCCTGC ACCTGGATGG GGGTCCCTGT GGGTCAAATT
 3951 GGGGGGAGGT GCTGTGGGAG TAAATACTG AATATATGAG TTTTTCAGTT
 4001 TTGAAAAAAA AAAAAAAAAA AAAAAAAAAA

FIGURE 51

GCAGGCTGCTCTCTGCTGCGCAGTGGGAAGTCTTGGCCCCGGLACCCCCGGATGCC
 1 -----+-----+-----+-----+-----+ 60
 CTTCCGACCGCAGGACGACGCTGCACCCCTTGGGACCGGGGCGGTGGGGCGCTACGG

a A A L R P A A H V G S P G F G H P R D A -
 b Q K C V L L R T W E A L A P A T P A M P -
 c S A A S C C A R G K P W F R P P F R C R -

CGCGCTCCCGCTGCGGAGCGCTGCGCTCCCTGCTGCGCAGCCACTACCGCGAGTACT
 61 -----+-----+-----+-----+-----+ 120
 CGCGGAGGGGCGACGCTCGGCGACGCGAGGGACGAAGCGTGGTGATGGCGCTCCACGA

a A R S P L F S R A L P A A Q P L P R G A -
 b R A P K C R A V R S L L R S H Y R E V L -
 c A L P A A E P C A P C C A A T T A R C C -

CGCGCTGCCACGTTCTGCTGCGGCGCTGGGGCCCCAGGGCTGGCGCTGGTGCGAGCGGG
 121 -----+-----+-----+-----+-----+ 180
 CGCGGACCGGTGCAAGCACGCGCGGACCCCCGGGTTCGACCGCCGACCAGTCCGGCTC

a A A G H V R A A P G A P G L A A G A A R -
 b P L A T F V R R L G P Q G W R L V Q R G -
 c R W P R S C G A W G P R A G G W C S A G -

GGACCGGGCGCTTTCCCGCGNTGGTGGCCCCANTGCTGGTGTGCGTGGCTGGGANGN
 181 -----+-----+-----+-----+-----+ 240
 CCTGGGCGCGGAAAGGGCGCCNACCACGGGTNACGNACCACGCGACGGCACCCCTNEN

a G P G G F P R ? G G P ? ? G V R A L G ? -
 b D P A A F R A ? V A ? C ? V C V P W ? ? -
 c T R R L S A R W W P ? A W C A C P G ? ? -

ANGGNGCCCCCGCTGCGCCCCCTTCCTCCCGCCAGGTGTCTGCTGAANGANGCTGGTGGC
 241 -----+-----+-----+-----+-----+ 300
 TNCCGNCGGGGGCGCGGGGAGGAAGGCGGTCCACAGGACGGACTTNTCTNGACCAAG

a ? A A F R R P L L P P C V L P E ? ? G G -
 b ? ? F P A A P S F R Q V S C L ? ? L V A -
 c G ? P P F P P P S A R C P A ? ? W W P -

CGAGTGTGTCANANGCTGTGGGANCCCCCGCGAANAACGTGCTGGCTTCCGCTTCCG
 301 -----+-----+-----+-----+-----+ 360
 GGCTCACGACTTNTNGACAGCTNGCGCGCGCTTNTTGCACGACCGAAGCGGAAGCG

a P S A A ? A V R ? R R E ? R A G L R L R -
 b R V L ? ? L C ? R G A ? N V L A P C P A -
 c E C C ? ? C A ? A A R ? T C W P S A S R -

GCTGCTGAGGGGGGCGGGGGGGCCCCCGACCCCTTACCCACCGGTGGCGAGCTA
 361 -----+-----+-----+-----+-----+ 420
 CGACGACCTGCCCCGGGCGCCCCGGGGGGGTCGGGAAGTGGTGGTGGCACCGGTGGAT

a A A G R G P R G P P R G L H H Q R A Q L -
 b L L G G A R G G P P E A F T T S V R S Y
 c C W T G P A G A P F R P S P P A C A A T -

[illegible]

[illegible]



	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

FIGURE 51 (cont.)

[illegible]

[illegible]

T I S T G P G A P S C C V C G F R T R K -
R Y F Q G L A H L R A A C A G P G P A A -
D I H S A W R T F V L R V R A Q D P P P -

1. S C T L S R W M * R A R T T F S F R T -
 * A V L C Q G G C D G R V R H H P P G Q
 E L Y F V K V D V T G A Y D T I P Q D R -

A G S R R S S P A S S N P R T R T A C V G -
 B A H G G H R Q H H Q T F E H V L R A S V -
 C L T E V I A S I I K P Q N T Y C V R R Y -

a M P W S R R P P M G T S A R P S R A T S -
b C R G P E C R P W A R P Q G L Q E F R L -
c A V V Q K A A H G H V R K A F K S H V S

J L P - Q T S S R T C D S S W L T C R ? T -
 b Y L D R P P A V H A T V R G S P A G ? Q -
 c T I T D L Q P Y M R Q F V A H L Q ? N S -

A R * G M P S S S S R A P P * M R P A V -
 P A E G C R R H R A E L L P E * G Q Q W -
 P L R D A V V I E O S S S L N E A S S G

A S S T S S Y A S C A T T P C A S G A S -
 P L R R L P T L H V P P R R A H Q G Q V -
 L F D V F L R F M C H H A V R T R G K S

[illegible]

a	a	a	a	a	a
b	b	b	b	b	b
c	c	c	c	c	c

H S R L G G T C V A N S L G S C G * S V T
 L Q G W E E H A S Q T L W G L A A E V S Q
 C K A G R N M R R E L F G V I R I K C H S -

A C F W I C R * T A S R R C A P T E T R -
P V S C F A G E Q P P D G V H Q H L Q D -
L F L D L Q V N S L Q T V C T N I Y K I -

a S S C C R R T G F T H V C C S S H F I S -
b F F A A G V Q V S R M C A A A P I S S A -
c L L L Q A Y R F H A C V L Q L P F H Q Q -

A K P G R T P H F S C A S S L T R P F S A -
 B S L E E P H I F P A R H L * H G L P L L
 C V W K N P T F F L R V I S D T A S L C Y

a T P S * K F R T Q G C E W G P R A F P A -
b L H F F S Q E R R D V A G G Q G R R R P -
c S I L K A K N A G M S L C A K C A A G P -

A L C P P P P C S G C A T E H S C S S * L -
 B S A L R G R A V A V P P S I P A Q A D S -
 C L P S E A V Q W L C H Q A F L L K L T R

a D T V S P T C H S W G H S G Q F R R S .
b T P C H L R A T P G V T Q D S P D A A E .
c H R V T Y V F L L G S L E T A Q T Q L S

FIGURE 51 (cont.)

GTGGGAAGCTCCGGGGAAGAGGCTGACTGCGCTGGAGGCGCGAGCCACCCGACCTGG
 3361 ----- 3420
 CAGCGCTTCGAGGGGCGCGCTGCTGCGACTGACGGGACCTCCCGCGCTCGGCTGCGCGTGAGG

 A V G S S R G R R * L F W R P Q F T R H C -
 B S E A P G D D A D C P G G R S Q P G T A -
 C R K L P G T T L T A L E A A A N P A L P -

 CCTCAGACTTCAGAGCCATCTTGGACTGATGCGACCTGCGCCACAGCCAGGCGAGAGCA
 3421 ----- 3480
 GGAATCTGAAAGTTCTGCTAGGACCTGACTACCGGTGGGGCGGCTGCTCGCTCGCGCTCTCTCT

 A P Q T S E P S W T D G H P F T A R P R A -
 B L R L Q D H P G L M A T R P Q F G R E Q -
 C S D F K T I L D * W P F A H S Q A E S R -

 GACACCAGCAGCTCTCTCAAGCGCGGCTCTAGCTCCAGGGAGGGAGGGCGCGCCACAC
 3481 ----- 3540
 CTGTGCTGCTGGGACAGTCCGGCGCGAGATGACAGGGTCCCTCCCTCCCGCGCGGCTG

 A D T S S F V T P G S T S Q G G R G G P H -
 B T F A A L S R R A L K P R E G G A A H T -
 C H Q Q P C H A G L Y V P G R E G R F T F -

 CCAGGCGCGGACCGGCTCGAGCTCAGCGCTGAGTGAGTGTGTTGGCGAGGGCTGCATGT
 3541 ----- 3600
 GGTCCGGGCGTGGCGACCTCAGACTCCGACTCACTCACAACCGGCTCCGAGGTACA

 A P G P H R W E S E A * V S V W P R P A C -
 B Q A R T A G S L R P E * V F G R G L H V -
 C K P A P L G V * G L S E C L A E A C M S -

 CCGGCTGAAGGCTGAGTGTGCGGCTGAGGCTTACGCTAGTCTCCACCCACCGGCTGAGT
 3601 ----- 3660
 GCGGACTTCCGACTCAGAGGCGGACTCCGACTCGCTCAGAGGTGGTTCCGACTTAC

 A P A E G * V S G * G L S E C P A K C * V -
 B R L F A E C P A E A * A S V Q P R A E C -
 C G * R L S V R L R P E R V S S Q G L S V -

 TTCAGTACAGCTGCGGCTCTTCACTTCCCGACAGGCTGCGGCTCGGCTCCACCCACGGG
 3661 ----- 3720
 AGGTGCTGTGGAGCGGAGAGCTGAAGCGCTGTCCGACCGGAGCGGAGGTGGGTTCCCG

 A S S T P A V F T S P Q A G A R L H P R A -
 B P A H L P S S L P H R L A L G S T P G P -
 C Q H T C R L H F P T G W E S A P P Q G Q -

 AGCTTTTCTCAGCAAGAGCGCGGCTTCCACTCCCGACATAGGAATAGTTCATCCCGAGA
 3721 ----- 3780
 TCGAAAVGAGTGTGCTCGGCGCGAAGGTGAGGGGTGTAATCTTATCAGCTAAGGCTCT

 A S F S S P G A R L P L P T * E * S T P R
 B A P P H Q E F G F H S P H R N S P S P D -
 C L F L T R S P A S T P H I G I V H P Q T -

3361 3420 3481 3540 3601 3660 3721 3780

F A I V H P S P C P P L P S T P T I Q V -
 S S L F T P P P A L L C L P P P P S R W -
 P H C S P L A L P S F A F H P H H P G G -

A T L E R T L G A L G I W S D Q R C A L -
 D E F E G P W E L W E F G V T K G V P C -
 C D F E E D F G S S C N L E P K V C L P V -

A Y T G E D P A P G W G S L W V K L G G C
B T Q A R T L H L D G G P C G S N W G E V
C H R R G P C T W M C V P V G Q I G G E C

A V G V K Y * I Y E F F S F E K K K K K
L W E * N T E Y M S F S V L K K K K K K
C G S K I L N I * V F Q F * K K K K K K

a	K	K	K	-
b	K	K		-
c		K	K	-

[illegible]

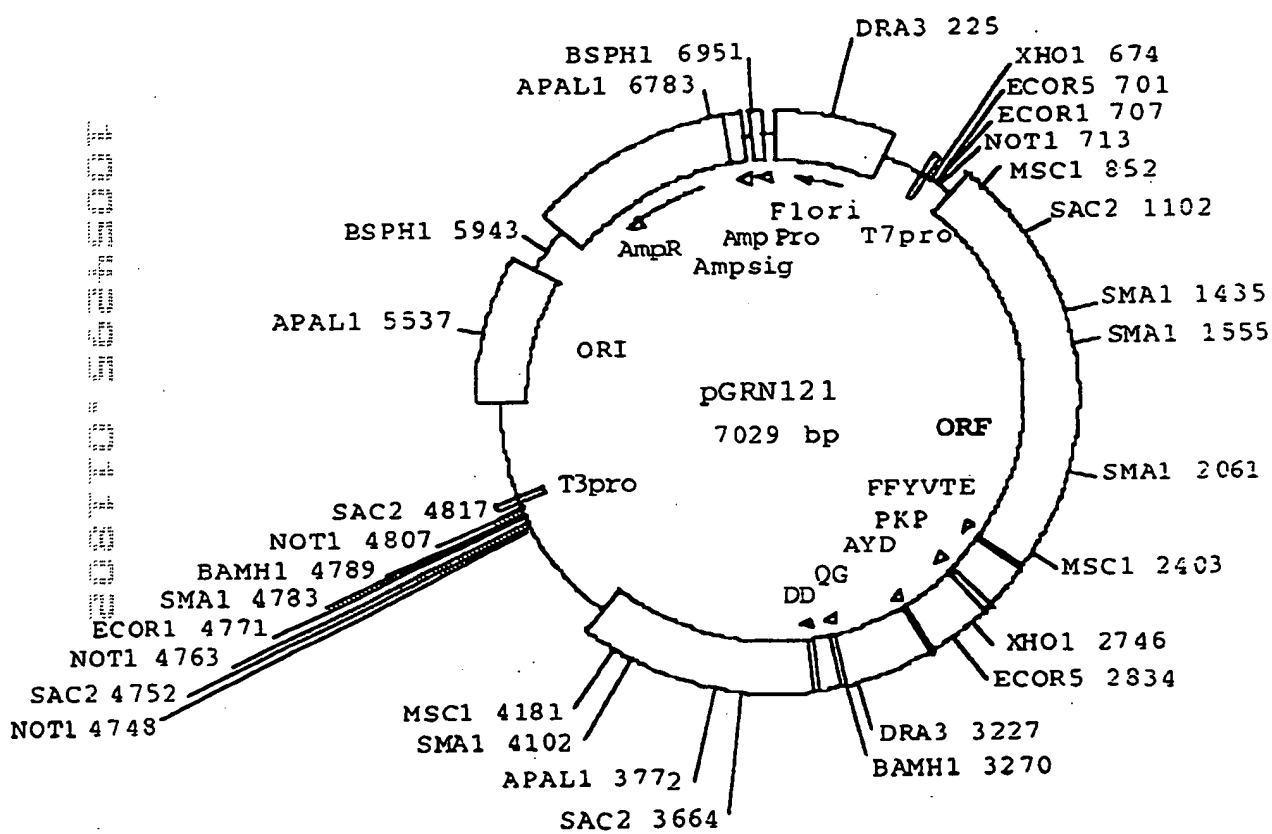
[illegible]

FIGURE 53

1
met
GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10
pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20 30
his tyr arg glu val leu pro leu ala thr phe val arg arg leu
CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

40
gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50 60
phe arg ala leu val ala gln cys leu val cys val pro trp asp
TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

70
ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80 90
leu lys glu leu val ala arg val leu gln arg leu cys glu arg
CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

100
gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110 120
ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

FIGURE 53 (cont.)

			140										150			
trp	gly	leu	leu	leu	arg	arg	val	gly	asp	asp	val	leu	val	his		
TGG	GGG	CTG	CTG	CTG	CGC	CGC	GTG	GGC	GAC	GAC	GTG	CTG	GTT	CAC		
								160								
leu	leu	ala	arg	cys	ala	leu	phe	val	leu	val	ala	pro	ser	cys		
CTG	CTG	GCA	CGC	TGC	GCG	CTC	TTT	GTG	CTG	GTG	GCT	CCC	AGC	TGC		
			170											180		
ala	tyr	gln	val	cys	gly	pro	pro	leu	tyr	gln	leu	gly	ala	ala		
GCC	TAC	CAG	GTG	TGC	GGG	CCG	CCG	CTG	TAC	CAG	CTC	GGC	GCT	GCC		
								190								
thr	gln	ala	arg	pro	pro	pro	his	ala	ser	gly	pro	arg	arg	arg		
ACT	CAG	GCC	CGG	CCC	CCG	CCA	CAC	GCT	AGT	GGA	CCC	CGA	AGG	CGT		
			200											210		
leu	gly	cys	glu	arg	ala	trp	asn	his	ser	val	arg	glu	ala	gly		
CTG	GGA	TGC	GAA	CGG	GCC	TGG	AAC	CAT	AGC	GTC	AGG	GAG	GCC	GGG		
								220								
val	pro	leu	gly	leu	pro	ala	pro	gly	ala	arg	arg	arg	gly	gly		
GTC	CCC	CTG	GGC	CTG	CCA	GCC	CCG	GGT	GCG	AGG	AGG	CGC	GGG	GGC		
			230											240		
ser	ala	ser	arg	ser	leu	pro	leu	pro	lys	arg	pro	arg	arg	gly		
AGT	GCC	AGC	CGA	AGT	CTG	CCG	TTG	CCC	AAG	AGG	CCC	AGG	CGT	GGC		
								250								
ala	ala	pro	glu	pro	glu	arg	thr	pro	val	gly	gln	gly	ser	trp		
GCT	GCC	CCT	GAG	CCG	GAG	CGG	ACG	CCC	GTT	GGG	CAG	GGG	TCC	TGG		
			260											270		
ala	his	pro	gly	arg	thr	arg	gly	pro	ser	asp	arg	gly	phe	cys		
GCC	CAC	CCG	GGC	AGG	ACG	CGT	GGA	CCG	AGT	GAC	CGT	GGT	TTC	TGT		
								280								
val	val	ser	pro	ala	arg	pro	ala	glu	glu	ala	thr	ser	leu	glu		
GTG	GTG	TCA	CCT	GCC	AGA	CCC	GCC	GAA	GAA	GCC	ACC	TCT	TTG	GAG		

FIGURE 53 (cont.)

290 300
gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

310
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

320 330
trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

350 360
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

380 390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

410 420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

FIGURE 53 (cont.)

440 450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

470 480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

500 510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

530 540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

560 570
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

580
arg leu phe phe tyr arg pro ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG CCG AGT GTC TGG AGC AAG TTG CAA AGC

590 600
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

FIGURE 53 (cont.)

610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

620
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

650
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

680
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

710
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

740
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

750
his gly his val arg lys ala phe lys ser his val ser thr leu
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC TCT ACC TTG

FIGURE 53 (cont.)

770														780	
thr	asp	leu	gln	pro	tyr	met	arg	gln	phe	val	ala	his	leu	gln	
ACA	GAC	CTC	CAG	CCG	TAC	ATG	CGA	CAG	TTC	GTG	GCT	CAC	CTG	CAG	
790															
glu	thr	ser	pro	leu	arg	asp	ala	val	val	ile	glu	gln	ser	ser	
GAG	ACC	AGC	CCG	CTG	AGG	GAT	GCC	GTC	GTC	ATC	GAG	CAG	AGC	TCC	
800															
ser	leu	asn	glu	ala	ser	ser	gly	leu	phe	asp	val	phe	leu	arg	
TCC	CTG	AAT	GAG	GCC	AGC	AGT	GGC	CTC	TTC	GAC	GTC	TTC	CTA	CGC	
810															
phe	met	cys	his	his	ala	val	arg	ile	arg	gly	lys	ser	tyr	val	
TTC	ATG	TGC	CAC	CAC	GCC	GTG	CGC	ATC	AGG	GGC	AAG	TCC	TAC	GTC	
820															
gln	cys	gln	gly	ile	pro	gln	gly	ser	ile	leu	ser	thr	leu	leu	
CAG	TGC	CAG	GGG	ATC	CCG	CAG	GGC	TCC	ATC	CTC	TCC	ACG	CTG	CTC	
830															
cys	ser	leu	cys	tyr	gly	asp	met	glu	asn	lys	leu	phe	ala	gly	
TGC	AGC	CTG	TGC	TAC	GGC	GAC	ATG	GAG	AAC	AAG	CTG	TTT	GCG	GGG	
840															
ile	arg	arg	asp	gly	leu	leu	leu	arg	leu	val	asp	asp	phe	leu	
ATT	CCG	CGG	GAC	GGG	CTG	CTC	CTG	CGT	TTG	GTG	GAT	GAT	TTC	TTG	
850															
leu	val	thr	pro	his	leu	thr	his	ala	lys	thr	phe	leu	arg	thr	
TTG	GTG	ACA	CCT	CAC	CTC	ACC	CAC	GCG	AAA	ACC	TTC	CTC	AGG	ACC	
860															
leu	val	arg	gly	val	pro	glu	tyr	gly	cys	val	val	asn	leu	arg	
CTG	GTC	CGA	GGT	GTC	CCT	GAG	TAT	GGC	TGC	GTG	GTG	AAC	TTG	CGG	
870															
lys	thr	val	val	asn	phe	pro	val	glu	asp	glu	ala	leu	gly	gly	
AAG	ACA	GTG	GTG	AAC	TTC	CCT	GTA	GAA	GAC	GAG	GCC	CTG	GGT	GGC	
880															
thr	ala	phe	val	gln	met	pro	ala	his	gly	leu	phe	pro	trp	cys	
ACG	GCT	TTT	GTT	CAG	ATG	CCG	GCC	CAC	GGC	CTA	TTC	CCC	TGG	TGC	
890															
900															
910															
920															
930															

FIGURE 53 (cont.)

940
gly leu leu leu asp thr arg thr leu glu val gln ser asp tyr
GGC CTG CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC

950
ser ser tyr ala arg thr ser ile arg ala ser val thr phe asn
TCC AGC TAT GCC CGG ACC TCC ATC AGA GCC AGT GTC ACC TTC AAC

960
arg gly phe lys ala gly arg asn met arg arg lys leu phe gly
CGC GGC TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG

970
val leu arg leu lys cys his ser leu phe leu asp leu gln val
GTC TTG CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG

980
asn ser leu gln thr val cys thr asn ile tyr lys ile leu leu
AAC AGC CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG

990
leu gln ala tyr arg phe his ala cys val leu gln leu pro phe
CTG CAG GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT

1000
his gln gln val trp lys asn pro thr phe phe leu arg val ile
CAT CAG CAA GTT TGG AAG AAC CCC ACA TTT TTC CTG CGC GTC ATC

1010
ser asp thr ala ser leu cys tyr ser ile leu lys ala lys asn
TCT GAC ACG GCC TCC CTC TGC TAC TCC ATC CTG AAA GCC AAG AAC

1020
ala gly met ser leu gly ala lys gly ala ala gly pro leu pro
GCA GGG ATG TCG CTG GGG GCC AAG GGC GCC GCC GGC CCT CTG CCC

1030
ser glu ala val gln trp leu cys his gln ala phe leu leu lys
TCC GAG GCC GTG CAG TGG CTG TGC CAC CAA GCA TTC CTG CTC AAG

1040
leu thr arg his arg val thr tyr val pro leu leu gly ser leu
CTG ACT CGA CAC CGT GTC ACC TAC GTG CCA CTC CTG GGG TCA CTC

1050
1060
1070
1080
1090

FIGURE 53 (cont.)

1100 1110
arg thr ala gln thr gln leu ser arg lys leu pro gly thr thr
AGG ACA GCC CAG ACG CAG CTG AGT CGG AAG CTC CCG GGG ACG ACG

1120
leu thr ala leu glu ala ala ala asn pro ala leu pro ser asp
CTG ACT GCC CTG GAG GCC GCA GCC AAC CCG GCA CTG CCC TCA GAC

1130 1132
phe lys thr ile leu asp OP
TTC AAG ACC ATC CTG GAC TGA TGGCCACCCGCCACAGCCAGGCCGAGAGCAGA

CACCAGCAGCCCCTGTCACGCCGGGCTCTACGTCCCAGGGAGGGAGGGCGGCCACACCC
AGGCCCGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCC
GGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTC
CAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCCAGGGCCAG
CTTTTCYTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATCCCCAGATT
CGCCATTGTTACCCYTCGCCCTGCCYTCCTTTGCCTTCCACCCCCACCATCCAGGTGGA
GACCCTGAGAAGGACCCTGGGAGCTCTGGAATTTGGAGTGACCAAAGGTGTGCCCTGTA
CACAGGCGAGGACCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGC
TGTGGGAGTAAAATACTGAATATATGAGTTTTTCAGTTTTGRAAAAAAAAAAAAAAAAAAA
AAAAAAAAAA

FIGURE 54

